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LOCUS Enterococcus faecalis polynucleotides and polypeptides.
DEFINITION
ACCESSION BD193668
VERSION BD193668.1 GI:33003407
KEYWORDS JP 2002529046-A/262.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 5277)
AUTHORS Kunsch, C.A., Dillon, P.J. and Barash, S.C.
TITLE Enterococcus faecalis polynucleotides and polypeptides
JOURNAL Patent: JP 2002529046-A 262 03-SEP-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2002529046-A/262
PD 03-SEP-2002
PF 04-MAY-1998 JP 1998548302
PR 06-MAY-1997 US 60/044031,16-MAY-1997 US 60/046555 PR
14-NOV-1997 US 60/066009
PI CHARLES A KUNSCH, PATRICK J DILLON, STEVEN C BARASH PC
C12N15/31, C07K14/315, C07K16/12, C12Q1/68
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CC Topology: Linear;
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DB	1106	CACGCGTTACAAAATCTCGACGCTGATGAATTGATTTTATTATTCCAAATGAATCCTCAA	1165
QY	121	CAATTTATTCAAGAAAGTGCTAATCATAAACGCTTTTTTTTGCAGAGCTTAGCCTCGTTCAAA	180
DB	1166	CAATTTATTCAAGAAAGTGCTAATCATAAACGCTTTTTTTTGCAGAGCTTAGCCTCGTTCAAA	1225
QY	181	GAACGAATCGATCAAGAGGCACATTTTACAAATCATGTCGCGCAACCAATTAGATTTATTT	240
DB	1226	GAACGAATCGATCAAGAGGCACATTTTACAAATCATGTCGCGCAACCAATTAGATTTATTT	1285
QY	241	TCACGTTTGAAACGCAAAATTACCGGATTTGCGAGGCCATTTTATTTAATGAAGATACCTGT	300
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73	Db	CACGCGTTACAAAATTTCTGCAGCTGATGAATTTATTTATTTCCAAATGAATCCTCAA	132
121	Qy	CAATTTATTCAGAAAGTGCTAATCATACGCTTTTTTTTCGACGCTTAGCTCGTTCAA	180
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LOCUS
DEFINITION Sequence 1313 from patent US 6617156.
ACCESSION AR395298
VERSION AR395298.1 GI:40123765
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
ORIGIN

Unknown.
Unclassified.
1 (bases 1 to 609)
Doucette-Stamm,L.A. and Bush,D.
Nucleic acid and amino acid sequences relating to Enterococcus
faecalis for diagnostics and therapeutics
Patent: US 6617156-A 1313 09-SEP-2003;
Location/Qualifiers
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Matches 608; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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LOCUS
DEFINITION Sequence 3604 from Patent WO0228891.
ACCESSION AX416613
VERSION AX416613.1 GI:21449070
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
ORIGIN

Listeria monocytogenes ATCC 19115
Listeria monocytogenes ATCC 19115
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Kunst,F. and Glaser,P.
Listeria inocua, genome and applications
Patent: WO 0228891-A 3604 11-APR-2002;
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Location/Qualifiers
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Best local Similarity 61.6%; Pred. No. 6.2e-93;		Matches 883; Conservative 0; Mismatches 536; Indels 15; Gaps 2;	
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Qy	841	CCACAACAAAAGAGGAGCTATTCAAGAAAAATTTTCGTTATTTTCAATGGACAAATGAC	900
Ds	1066	CCTAACCAAAAACAGCCGATCCAGAAAATTTATCGTTTTTATGATGGGAAAATAAC	1125
Qy	901	CCAGAAATGTTTGTCAAGTGGCAAAAAGGGAGACGGGGTACCTCTATAATTTGATGCCGA	960
Ds	1126	CGCGAATATTTCAAAGCGTGGCAAGAGGGAAGACTGGTTTCCCGCTCGTTGATGCGGCG	1185
Qy	961	ATGCGACAACTGAATCAACTGGTTGGATGCACAATCGCTTTAAGAAATGATTCTGCTCT	1020
Ds	1186	ATGCGCCAGTTTGAAGAAACTGGTTGGATGCATATCGACTAAGAATGATTACGCGCTCC	1245
Qy	1021	TTTTTAGTAAAAATTTACACATCGATTGGGCTGGGTGAAAAATACCTTTCAAAAAATG	1080

Ds	1246	TTTTTAACAAAAGATTTGCTGATTGATTGGCGTTTTTGGCGAAAAGTAGTATTTTCAACAAATG	1305
Qy	1081	TTGATTGACTATGATGCTGCAATATATATCGTGGCTGGCAATGGGCTGCTTCAACAGGA	1140
Ds	1306	CTGATTGATTATGATCTCGAGTAATATTGGTGGCTGGCAATGGGCGGCTTGCATGGA	1365
Qy	1141	ACGAGCGCTGCTCCCTTATTTTTCGGATTTTAAATCCAAATTTCCAGTCAAAAAATTTGAT	1200
Ds	1366	ACGATGCGGTGCATATCTTTAGATTTTCAACCAACGACACATCACAAAAATTTGAT	1425
Qy	1201	AATGACGGCCAGTTCATCAAAAAATATGTTCCAGAACTTAAAGCAAGTCCCAAAAAGTAT	1260
Ds	1426	TCGACTGGGAAATTTATTCGAAAATATGTAAGAGAGTTAGCGAATCTACCTGATAAATAT	1485
Qy	1261	ATTATCAACCAAACTTAATGAACGAGCCCTTCAACAGCAATATCATGTACATTTAGGA	1320
Ds	1486	ATTATCAACCAAAAAATGTGAGAACTGAGCAGAAAGAGCATGGCTTGTGTAGGA	1545
Qy	1321	GAAAAATTTATCCAAAACCCATTGTCGATTATGATCAAGTAAAAAACAACCAATTTGTTCTA	1380
Ds	1546	AAAGACTATCCATTTCCGATAGTTGACCATAAAGACGACGGAATTTAGCCATTTGACGC	1605
Qy	1381	TATGAACGCGAGCAAGAAATTCATCAAGAAATGAACAATCCAAAGTTTCAATAA	1434
Ds	1606	TACGAGTTTAGCAAGAGCATTCTAGGGAAATATATAGATAATGAGTCAATCA	1659
RESULT 6			
LOCUS	AE017324	290242 bp	DNA linear BCT 30-APR-2004
DEFINITION	Listeria monocytogenes str. 4b F2365, section 3 of 10 of the complete genome.		
ACCESSION	AE017324	AE017262	
VERSION	AE017324.1	GI:46880047	
KEYWORDS	Listeria monocytogenes str. 4b F2365		
SOURCE	Listeria monocytogenes str. 4b F2365		
ORGANISM	Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.		
REFERENCE	1 (bases 1 to 290242)		
AUTHORS	Nelson, K.E., Fouts, D.E., Mongodin, E.F., Ravel, J., DeBoy, R.T., Kolonay, J.F., Rasko, D.A., Angiuoli, S., Gill, S.R., Paulsen, I.T., Peterson, J.D., White, O., Nelson, W.C., Nierman, W.C., Beanan, M.J., Brinkac, L.M., Daugherty, S.C., Dodson, R.J., Durkin, A.S., Madupu, R., Haft, D.H., Selengut, J., Van Aken, S., Khouri, H., Fedorova, N., Forberger, H.A., Tran, B., Kacharou, S., Wondolring, L.D., Uhlrich, G.A., Bayles, D.O., Luchansky, J.B. and Fraser, C.M.		
TITLE	Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species		
JOURNAL	Nucleic Acids Res. 32 (8), 2386-2395 (2004)		
PUBMED	15115801		
REFERENCE	2 (bases 1 to 290242)		
AUTHORS	Nelson, K.E., Fouts, D.E., Mongodin, E.F., Ravel, J., DeBoy, R.T., Rasko, D.A., Kolonay, J.F., Angiuoli, S., Gill, S.R., Paulsen, I.T., Peterson, J.D., White, O., Nelson, W.C., Nierman, W.C., Van Aken, S.E., Khouri, H.M., Fedorova, N.B., Forberger, H.A., Tran, B. and Fraser, C.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-FEB-2004) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA		
FEATURES	Location/Qualifiers		
source	1. .290242		
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CDS	83. .1354		
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gene		Query Match Best Local Similarity 61.4%; Score 523.2; DB 1; Length 290242; Matches 881; Conservative 0; Mismatches 538; Indels 15; Gaps 2;	
Qy	1	ATGAAAAGAGTAATATGCTTTAGACGTGATTTACGATTACAGGATAATAAGCAATTAGCA 60	
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Qy	61	CACGGTTACAAAATCTCGAGCTGATCAATGATTTTATTTATTTCCAAATGAATCCTCAA 120	
Ds	54074	CATGC-----TTGTAAGAGAGAACGATTTGCTTTTGTATTTCAGTAAATCCAGCA 54124	
Qy	121	CAATTTATTCAAGAAAGTGCTAATCATAAACGCTTTTTTTCGAAGCTTAGCCTCGTTCAAA 180	
Ds	54125	CAGTTCATCAGAGNAGTCTTAGCCACCAAGCTTTTTTTCGAAGTGGCTCATTTTAAAG 54184	
Qy	181	GAACGAATCGATCAAGAGGCAATTTACAAATCATGTCGGCGAACCAATAGATTTATTT 240	
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Qy	241	TCAGTTTGAACGCAANTTACCCGATGGCAGGCCATTTATTTTATGAAGTACTTGT 300	
Ds	54245	CAACAACTTAAAGATTTCGCTACCAAGCTGGGATAAAGTTTATTTCAACCGTGATGAAACA 54304	
Qy	301	GGCTTTGGGCAAGCGGACAGCAAGCTATGGCTTTTTTGAAGAAATAATATTTCAG 360	
Ds	54305	GGATACGAGCAAGCGGATGAGCGCGCAAGGTTCTTTGACGACAAAANAATCGAG 54364	
Qy	361	TCCTTTCTTTTCAAGATGCCATTTTGATGGCTCTGAAGAAATAAGAGAACGATGGC 420	
Ds	54365	GTTCAGGCTTCCACGATAGTTATCTTCATTCAGCGGAAGAAGTAAAGAAATCTCCAAACA 54424	
Qy	421	AGCAAGTACCAAGTGTTCACGCCCTATTACAAATAATGGAAGAGCGCCCTAAGAAACA 480	
Ds	54425	GAATACTATAAAATTTTACGCCCTTATTATAAAATATGGCCGGAAGAAATAAAGAACG 54484	
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Qy	721	GAACTTCGATTCGCACCATTTGGCAAGAGCTTGCATCTGTGCCCTTCCTAGCTTAAAGTAA 780	
Ds	54719	GAAATCTCGATTCCGACGATTTGGCAGTCACTTCAAGAAACAGAAGCAACAGAAGGACGA 54778	
Qy	781	GAAACCTTCAAAAAGATTAGCTTGGCGCACTTTACATATATGATCTAGTGCCTTT 840	
Ds	54779	GCTACATTTGAAAAGAACTTTGTGTGGCGCACTTTTATAATATGATTTAGTTTCTTTT 54838	
Qy	841	CCACAACAAAAGAGAGACTATTCAAGAAAAATTTTCGTTTATTTCAATGACAAATGAC 900	

Ds	54839	CCTAACCAAAAAACGAGCGGATCCAGAAAAATATTTCGTTTTTATGAAATGGGAAAAATAAC	54898
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Ds	54899	CGTGAATATTTTCAAGCGTGGCAAGGAAAGGAACTGGTTTCCCGCTCGTGTGATGGCGG	54958
Qy	961	ATCGGCAACTGTAATCAAACTGGTGGATGCACAAATCGCTTAAAGAAATGATTACTGCTCT	1020
Ds	54959	ATCGCCAGTGTGAAGAAACTGGTGGATGCATAATCGACTAAGATGATTAGCGGCTCC	55018
Qy	1021	TTTTTTAGTTAAAAATTTACACATCGAATGGCGTTGGGGTGAAGAAATATCTTTCAAAAAATG	1080
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Qy	1081	TTGATTGACTATGATGCTGCCAATATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA	1140
Ds	55079	CTGATTGATTATGATCTCGAGTAATATTGGTGGCTGGCAATGGGGGGCTTGCATCGGA	55138
Qy	1141	ACGGAGCTGTCCCTTATTTTCGGATTTTTTAATCCAATTTATCCAGTCAAAAAAATTTGAT	1200
Ds	55139	ACGGATGCGGTGCCATCTTTTAGGATTTTCAACCCACGACACAATCACAANAATTTGAT	55198
Qy	1201	AATGACGGCGAGTTTCATCAAAAAATATGTTCCAGAACTTAAAGCAAGTGCACAAAAGTAT	1260
Ds	55199	TCGACTGGGAAATTTTATTCGAAAAATATGTAAGAGAGTTAGCGAATCTACCTGATAAAT	55258
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Ds	55259	ATTTCATCAACCAAAAAATGTCCAGAACTGAGCAGAAAGAGCATGGCTTGTGTTAGGA	55318
Qy	1321	GAAAAATTCCAAAACCCATTGTCGATTATGTCATCAAGTAAAAAACAACATTTGTTCTA	1380
Ds	55319	AAAGACTATCCATTTCCGATAGTTGACCATAAAGACGCGGAATTAGCCATTTGACCATG	55378
Qy	1381	TATCAAGCGAGCAAGAAATTCATCAAGAAATCAACAATCCAAAGTTTCAATAA	1434
Ds	55379	TACGAGTTTAGCAAGAGCATTTCTAGGGAAATATATAGATAANTAGTCAATCA	55432
RESULT 7			
AL596165	249050 bp	DNA	linear BCT 16-APR-2005
LOCUS	Listeria innocua Clp11262 complete genome, segment 3/12.		
DEFINITION	Listeria innocua Clp11262 complete genome, segment 3/12.		
ACCESSION	AL596165		
VERSION	AL596165.1 GI:16412888		
KEYWORDS	.		
SOURCE	Listeria innocua		
ORGANISM	Listeria innocua		
REFERENCE	1		
AUTHORS	Glaser, P., Frangeul, L., Buchrieser, C., Rueniok, C., Amend, A., Baquero, F., Berche, P., Bloeker, H., Brandt, P., Chakraborty, T., Charbit, A., Chetouani, F., Couve, E., de Daruvar, A., Dehoux, P., Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L., Dussurget, O., Entian, K.D., Fsihi, H., Garcia-del Portillo, F., Garrido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T., Hauf, J., Jackson, D., Jones, L.M., Kaerst, U., Kref, J., Kuhn, M., Kunst, F., Kurapkat, G., Madueno, E., Maitournam, A., Vicente, J.M., Ng, E., Nedjari, H., Nordstiek, G., Novella, S., de Pablo, B., Perez-Diaz, J.C., Purcell, R., Remmel, B., Rose, M., Schluster, T., Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and Cosset, P.		
TITLE	Comparative genomics of Listeria species		
JOURNAL	Science 294 (5543), 849-852 (2001)		
PUBMED	11679669		
REFERENCE	2 (bases 1 to 249050)		
AUTHORS	Glaser, P., Frangeul, L. and Rueniok, C.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-JUL-2001) Glaser P., Institut Pasteur, Genomique des Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE		
COMMENT	E-mail: pglaser@pasteur.fr Phone: +33 (0)1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.		

FEATURES	source	Location/Qualifiers
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seq 4030: from 600001 to 949980
seq 4031: from 900000 to 1163020"

ORIGIN

Query Match 36.2%; Score 518.4; DB 6; Length 349980;
Best Local Similarity 61.2%; Pred. No. 5.1e-92;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

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QY 61 CACGGGTTACAAAATTCGCAGCTGATGATTTGATTTTATTATCCAAATGAATCCTCAA 120
DB 237875 CATGCTGTGAAGA-----AGAAGATTTAAATTTTGTATTATTCATAGTAATCCAGAA 237925
QY 121 CAATTTTATCAAGAAAGTGCTAATCATAAACGCTTTTTTGTCAAGCTTAGCCCTCGTTCAAA 180
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QY 181 GAACGAATCGATTCAAGAGCGACATTTACAAATCATGTCGGCGAACCATTAGATTTATTT 240
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AX417041 349980 bp DNA linear PAT 02-SEP-2002
LOCUS Sequence 4032 from Patent WO0228891.
DEFINITION
ACCESSION AX417041
VERSION AX417041.1 GI:21449651
KEYWORDS
SOURCE Listeria innocua
ORGANISM Listeria innocua
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE

1 Kunst, F. and Glaser, P.
Listeria innocua, genome and applications
Patent: WO 0228891-A 4032 11-APR-2002;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)

FEATURES

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Location/Qualifiers
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seq 4033: 0.600.001 to 0.949.980
seq 4034: 0.900.001 to 1.249.980
seq 4035: 1.200.001 to 1.549.980
seq 4036: 1.500.001 to 1.849.980
seq 4037: 1.800.001 to 2.149.980
seq 4038: 2.100.001 to 2.449.980
seq 4039: 2.400.001 to 2.749.980
seq 4040: 2.700.001 to 3.049.980
seq 4041: 3.000.001 to 3.011.208"

ORIGIN

Query Match 36.2%; Score 518.4; DB 6; Length 349980;
Best Local Similarity 61.2%; Pred. No. 5.1e-92;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;
QY 1 ATGAAAAGAGTAATATGTTTAGACGCTGATTTACGATTACAGGATAATAAAGCATTAGCA 60

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RESULT 10
AX417042 349980 bp DNA linear PAT 02-SEP-2002

LOCUS
DEFINITION Sequence 4033 from Patent WO0228891.
ACCESSION AX417042
VERSION AX417042.1 GI:21449652
KEYWORDS
SOURCE Listeria innocua
ORGANISM Listeria innocua
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE 1
AUTHORS Kunst, F. and Glaser, P.
TITLE Listeria innocua, Genome and applications
JOURNAL Patent: WO 0228891-A 4033 11-APR-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)

FEATURES
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seq 2058: 0.000.001 to 0.349.980
seq 4032: 0.300.001 to 0.649.980
seq 4033: 0.600.001 to 0.949.980
seq 4034: 0.900.001 to 1.249.980
seq 4035: 1.200.001 to 1.549.980
seq 4036: 1.500.001 to 1.849.980
seq 4037: 1.800.001 to 2.149.980
seq 4038: 2.100.001 to 2.449.980
seq 4039: 2.400.001 to 2.749.980
seq 4040: 2.700.001 to 3.049.980
seq 4041: 3.000.001 to 3.011.208"

ORIGIN

Query Match 36.2%; Score 518.4; DB 6; Length 349980;
Best Local Similarity 61.2%; Pred. No. 5.1e-92;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

Qy 1 ATGAAAGAGTATATGTTTAGACGTGATTTACGATTAAGGATTAAGGATTAAGGATTAAGCA 60
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AL591975 AL591824			
VERSION AL591975.1 GI:16409709			
KEYWORDS			
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ORGANISM Listeria monocytogenes			
REFERENCE 1 Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.			
AUTHORS			
Glaser, P., Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A.,			
Baquero, F., Berche, P., Bloeker, H., Brandt, P., Chakraborty, T.,			
Charbit, A., Chetouani, P., Couve, E., de Daruvar, A., Dehoux, P.,			
Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L.,			
Dussurget, O., Entian, K.D., Goebel, W., Gomez-Lopez, N., Hain, T.,			
Garrido, P., Gautier, L., Jones, L.M., Kaerst, U., Kref, J., Kuhn, M.,			
Hauf, J., Kurapkant, G., Madueno, E., Maitournam, A., Vicente, J.M.,			
Kunst, P., Jackson, D., Jones, L.M., Kaerst, U., Kref, J., Kuhn, M.,			
Ng, E., Nedjari, H., Nordsiek, G., Novella, S., de Pablo, B.,			
Perez-Diaz, J.C., Purcell, R., Remmel, B., Rose, M., Schlueter, T.,			
Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and			
Cossart, P.			
Comparative genomics of Listeria species			
Science 294 (5543), 849-852 (2001)			
11679669			
2 (bases 1 to 280050)			
Glaser, P., Frangeul, L. and Rusniok, C.			
Direct Submission			
Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des			
Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris			
Cedex 15, FRANCE			
E-mail: pglaser@pasteur.fr			
Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.			
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Qy	1201	AATGACGGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAAGCAAGTCCACAAAAAGTAT	1260
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LOCUS			
DEFINITION			
SEQUENCE			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Listeria monocytogenes			
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.			
REFERENCE			
1 Buchrieser, C., Frangeul, L., Couve, E., Rusniok, C., Fsihi, H.,			
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VERSION AX641666.1 GI:28474427
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Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria.
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AUTHORS
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Dehoux, P., Dussurget, O., Chetouani, F., Nedjari, H., Glaser, P.,
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Listeria monocytogenes genome, polypeptides and uses
Patent: WO 0101118-A 2856 11-APR-2001;
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AUTHORS Kunst,F. and Glaser,P.
TITLE Listeria inocua, genome and applications
JOURNAL Patent: WO 0228891-A 1690 11-APR-2002;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
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REFERENCE
AUTHORS

1 Telford, J., Masignani, V., margarit y Ros, I., Grandi, G., Fraser, C.
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Nucleic acids and proteins from streptococcus groups a b
Patent: WO 03093306-A 1139 13-NOV-2003;
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	166	11.6	544	2	BI263965
C 2	156.4	10.9	823	10	CL659411
C 3	145.4	10.1	841	10	C2547170
C 4	138.2	9.6	434	2	BE459864
C 5	137.4	9.6	760	8	DT043899
C 6	129	9.0	989	11	CNS0710N
C 7	116.8	8.1	787	8	DN981737
C 8	113.2	7.9	740	6	CD458345
C 9	111.6	7.8	991	11	CNS071TH
C 10	108.2	7.5	1063	9	BZ563216
C 11	107.6	7.5	773	10	CL692005
C 12	106.8	7.4	420	9	BZ893625
C 13	104.8	7.3	717	8	DT001226
C 14	104.6	7.3	748	3	BI311349
C 15	103.6	7.2	699	5	BO854812
C 16	102.4	7.1	649	6	CA989448
C 17	101	7.0	427	7	CO442739
C 18	100.8	7.0	393	7	CO067931
C 19	99.6	6.9	854	8	CV769258
C 20	99.4	6.9	645	6	CD924582
C 21	97.8	6.8	528	7	CN491610
C 22	97	6.8	1071	4	CNS0A821

23	96.4	6.7	615	1	AW309100
24	94	6.6	449	7	CO135296
25	92.2	6.4	798	8	CK714323
26	91.8	6.4	619	5	BQ392047
27	91.4	6.4	526	7	CO901104
28	90.8	6.3	733	5	BQ82562
29	90.2	6.3	607	8	CK487760
30	90.2	6.3	627	8	CK487761
31	89.8	6.3	795	8	CK471210
32	89.2	6.3	552	3	BI787441
33	89.2	6.2	601	5	BU082486
34	89.2	6.2	723	5	BQ863292
35	88.2	6.2	773	5	BQ861871
36	88.2	6.2	692	7	CV532994
37	87.6	6.1	906	5	BU916216
38	87.2	6.1	654	2	BE249224
39	87.2	6.1	690	2	BF631699
40	87	6.1	791	6	CB671067
41	87	6.1	792	6	CB671155
42	87	6.1	803	6	CB677310
43	86.5	6.0	825	6	CA765778
44	85.2	5.9	696	5	BQ860163
45			600	9	BZ893135

ALIGNMENTS

RESULT 1
BI263965/c
LOCUS
DEFINITION NF092B05PL1F1045 Phosphate starved leaf Medicago truncatula cDNA
clone NF092B05PL 5', mRNA sequence.
544 bp mRNA linear EST 18-JUL-2001
ACCESSION BI263965
VERSION BI263965.1 GI:14865752
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside 1; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 544)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library
JOURNAL Unpublished (2000)
COMMENT Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7320
Email: mjharrison@noble.org
Insert Length: 544 Std Error: 0.00
Plate: 092 row: B column: 05
Seq primer: TCACACGAGAACACGCTATGAC.
Location/Qualifiers
1. 544
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF092B05PL"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/note="lib=Phosphate starved leaf"
/clone="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."

FEATURES
source

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ORIGIN
Query Match      11.6%; Score 166; DB 2; Length 544;
Best Local Similarity 64.1%; Pred. No. 2.6e-30;
Matches 250; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 882 TATTCAATGGACAAATGACCCAGCAATGTTGTCAAGTGGCAAAAGGGAGAGCGGGTA 941
Db 503 TGTACAGTGGCAGAGCAATCCCGCACATTTACAGGCTGGGAGGAAGGCAAAACGGGATA 444
QY 942 CCCTATAATTTGATGCGCAATGCGACCACTGAATCAAACTGTTGGATGCAACATCGCTT 1001
Db 443 CCCGATTGTTGATGCGCTATGCGTCACTTAACAGCACTGGCTGGATGATACAGGCT 384
QY 1002 AAGAAATGATTACTGCTCTTTTATAGTTAAATTTACACATTCGATTTGGGCTTGGGGTGA 1061
Db 383 ACGGATGATTACAGCCAGTTTCTGGTGAAGATTTATGATCGACTGGCGCGAAGCGCA 324
QY 1062 AATAATCTTTCAAAAATGTTGATTGACTATGATGCTGCCAATAATATCGTGGCTGGCA 1121
Db 323 CGGATATTTGATGCGAGCTGATGATGGTGGTGGCAGCCCAATAACCGTGGCTGGCA 264
QY 1122 ATGGGCTGCTTCAACAGGAACGGACGCTGTCCCTTATTTTCGGATTTTAAATCCAAATTAT 1181
Db 263 GTGGGCGCTTCAACCGGAACCGATGACGCGCGTATTTTCGTATTTCAACCGCAAC 204
QY 1182 CCACTCAAAAATTTGATTAATGACGCGCGATTCATCAAAAATATGTTCCAGAACTTAA 1241
Db 203 CCAGGGCGAGAAATTTGATCATGAGGCGAGTTTATCCGCCAGTGGCTACCGGAACCTGCG 144
QY 1242 GCAGTGGCCACAAAGTATATTTCATCAACC 1271
Db 143 CGATGTGCCAGGAAAGTGGTGCAATGAGCC 114

RESULT 2
CL659411
LOCUS CL659411 823 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0134a_c11 - PRI0134a.B21 (823) Mixed stage fosmid library of P.
survey sequence.
ACCESSION CL659411
VERSION CL659411.1 GI:50143492
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
AUTHORS Neodiplogasteridae; Pristionchus.
TITLE Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
APPABD: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..823
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"

FEATURES
source
Location/Qualifiers
1..823
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"

ORIGIN
/note="Vector: pEpifos-5 Fosmid vector"

Query Match      10.9%; Score 156.4; DB 10; Length 823;
Best Local Similarity 62.6%; Pred. No. 7.1e-28;
Matches 244; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

QY 882 TATTCAATGGACAAATGACCCAGCAATGTTGTCAAGTGGCAAAAGGGAGAGCGGGTA 941
Db 151 TGTGCAAGTGGCAGAGCAATCCCGCACATTTACAGGCTGGCAGGAAGGCAAAACGGGATA 210
QY 942 CCCTATAATTTGATGCGCAATGCGACCACTGAATCAAACTGTTGGATGCAACATCGCTT 1001
Db 211 CCCGATTGTTGATGCGCTATGCGTCACTTAACAGCACTGGCTGGATGATACAGGCT 270
QY 1002 AAGAAATGATTACTGCTCTTTTATAGTTAAATTTACACATTCGATTTGGGCTTGGGGTGA 1061
Db 271 ACGGATGATTACAGCCAGTTTCTGGTGAAGATTTTGTGATCGACTGGCGCGAAGCGCA 330
QY 1062 AATAATCTTTCAAAAATGTTGATTGACTATGATGCTGCCAATAATATCGTGGCTGGCA 1121
Db 331 CGGATATTTGATGCGAGCTGATGATGGTGGTGGCAGCCCAATAACCGTGGCTGGCA 390
QY 1122 ATGGGCTGCTTCAACAGGAACGGACGCTGTCCCTTATTTTCGGATTTTAAATCCAAATTAT 1181
Db 391 GTGGGCGCTTCAACCGGAACCGATGACGCGCGTATTTTCGTATTTCAACCGCAAC 450
QY 1182 CCACTCAAAAATTTGATTAATGACGCGCGATTCATCAAAAATATGTTCCAGAACTTAA 1241
Db 451 CCAGGGCGAGAAATTTGACCGTGAGGCGAGTTTATTCGTCGATGGTTACCGGAGCTGCG 510
QY 1242 GCAGTGGCCACAAAGTATATTTCATCAACC 1271
Db 511 CGATGTGCCAGGAAAGTGGTGCAATGAGCC 540

RESULT 3
CZ547170/c
LOCUS CZ547170 841 bp DNA linear GSS 13-MAY-2005
DEFINITION SRAA-aad72c04.g1 Strongyloides ratti whole genome shotgun library
(SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.
ACCESSION CZ547170
VERSION CZ547170.1 GI:64682731
KEYWORDS GSS.
SOURCE Strongyloides ratti
ORGANISM Strongyloides ratti
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
AUTHORS Panagrolaimoidea; Strongyloidea; Strongyloidea.
TITLE Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D.,
Ritter,E., Martin,J., Wylie,I., Dante,M., Waterston,R.H.,
Clifton,S.W. and Wilson,R.
Genome Survey sequences from the rat parasitic nematode
Strongyloides ratti
JOURNAL Unpublished (2005)
COMMENT Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
Genomic DNA was provided by Fiona Thompson
(F.Thompson@bristol.ac.uk) and Mark Viney
(Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol,
UK.
Class: shotgun.
Location/Qualifiers
1..841
/organism="Strongyloides ratti"
/mol_type="genomic DNA"
/strain="Isotfemale line ED321 heterogonic"
/db_xref="taxon:34506"

FEATURES
source
Location/Qualifiers
1..841
/organism="Strongyloides ratti"
/mol_type="genomic DNA"
/strain="Isotfemale line ED321 heterogonic"
/db_xref="taxon:34506"
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RESULT 7
DN981737/c
LOCUS SV6 40E04_AV59_023 SV6 Solanum chacoense cDNA, mRNA EST 15-JUN-2005
DEFINITION DN981737
ACCESSION DN981737.1 GI:67769548
VERSION DN981737.1
KEYWORDS EST.
SOURCE Solanum chacoense (Chaco potato)
ORGANISM Solanum chacoense
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 787)
Germain,H., Rudd,S., Zotti,C., Caron,S., O'Brien,M., Chantha,S.-C.,
Legace,M., Major,F. and Matton,D.P.
A 6374 unigene set corresponding to low abundance transcripts
expressed following fertilization in Solanum chacoense Bitt., and
expression profile of 30 receptor-like kinases
Unpublished (2005)
Contact: Daniel P. Matton
Daniel P. Matton
Universite de Montreal
Institut de recherche en biologie vegetale, 4101 rue Sherbrooke
est, Montreal, QC, Canada, H1X 2B2
Tel: 5148723967
Fax: 5148729406
Email: dp.matton@umontreal.ca.
FEATURES
Source
1..787
/organism="Solanum chacoense"
/mol_type="mRNA"
/db_xref="taxon:4108"
/tissue_type="2-6 days post-pollination ovaries"
/dev_stage="Zygotic to globular embryo"
/lab_host="SOL"
/clone_lib="SV6"
/Note="Organ: Deparicarped ovary/ovules with placenta
tissue; Vector: pBS SK; Site 1: EcoRI; Site 2: XhoI;
Deparicarped ovaries were isolated from a compatible cross
between self-incompatible accessions having the S12S14
self-incompatibility alleles (G4 line as female) and
S1S13 self-incompatibility alleles (V22 line as male).
Those two lines were derived from the parental lines PI
458314 (which carries the S11 and S12 self-incompatibility
alleles) and line PI 230582 (which carries the S13 and
S14 alleles) obtained through the potato introduction
Station (Sturgeon Bay, WI). Plants were grown in
greenhouses under natural light, fruit collection took
place in the morning during summer (approx. 14h daylight),
and fruits were pooled from different plants. Total RNA
was isolated as described in EMBO J. 4: 2411-2418, 1985.
The poly A+ RNA was purified from the total RNA by
affinity chromatography using oligo dt agarose beads type
VII (Amersham). Mean clone length of the library was 1,5
kb."
ORIGIN
Query Match 8.1%; Score 116.8; DB 8; Length 787;
Best Local Similarity 65.2%; Pred. No. 5.4e-18;
Matches 172; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 882 TATTCAATGCAGCAATGACCCAGAAATGTTTGTCAAGTGGCAAAAGGGGAGACGGGTA 941
Db 265 TGTACAGTGGCAGAGCAATCCGCACATTTACAGGCCTGGCAGGAAGGCAAAACGGGATA 206
QY 942 CCTATAATTGATCGCGCAATGGGCAACTGATCAAACTGGTTGGATGTCACAAATCGCTT 1001
Db 205 CCGGATTGTTGATGCGCGCTATGCGTCAGCTTAACAGCACTGGCTGGATGCATTAACAGGCT 146
QY 1002 AGAATGATTACTGCTCTTTTACTTAAATTTTACATCGATTGGCGTTGGGGTGA 1061

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Db 145 ACGGATGATTACAGCCAGTTTTCTGTGAAAGATTTATTGATCGACTGGCGGAGCGGA 86
QY 1062 AAAATACTTTCAAAAAATGTTGATGACTATGATGTCGCCAATAATAATCGTGCTGGCA 1121
Db 85 GCATATTTCATGTCGAGCTGATTGATGCTGATTTGGCAGCAATAACGGTGGCTGGCA 26
QY 1122 ATGGGCTGCTTCAACAGGAACGGA 1145
Db 25 GTGGGCGCTTCAACCGGAACCGA 2
RESULT 8
CD458345 740 bp mRNA linear EST 14-JUN-2004
LOCUS CD458345
DEFINITION Fg08_12109 A Fg08 AAFc ECORC Fusarium graminearum complex_substrate
Gibberella zeae cDNA clone Fg08_12109, mRNA sequence.
ACCESSION CD458345
VERSION CD458345.1 GI:31373085
KEYWORDS EST.
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 740)
Watson,R.J., Heyes,R., Chapados,J., Couroux,P., Harris,L.J.,
Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,
Sprott,D. and Tinker,N.A.
A cDNA library prepared from Fusarium graminearum grown on a
complex plant substrate
Unpublished (2003)
Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.
FEATURES
Source
1..740
/organism="Gibberella zeae"
/mol_type="mRNA"
/db_xref="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg08_12109"
/tissue_type="Mycelium"
/dev_stage="Asexual"
/lab_host="E. coli DH10B"
/clone_lib="Fg08_AAFc_ECORC_Fusarium_graminearum_complex_s
ubstrate"
/Note="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."
ORIGIN
Query Match 7.9%; Score 113.2; DB 6; Length 740;
Best Local Similarity 55.3%; Pred. No. 4.2e-17;
Matches 260; Conservative 0; Mismatches 208; Indels 2; Gaps 2;
QY 807 GCGGACTTTTACAAATATGATCTATAGTGGCTTTCCACAAACAAAGAGGAGTATTCA 866
Db 40 GCGAGACTTTACAAACATGTTCTGTCAACTGGCCATAGCTCTGTATGAACAGCCCTTTA 99
QY 867 AG-AAAAATTTGTTTATTTCAATGGCAAAATGACCCAGAAATGTTTGTCAAGTGGCAA 925
Db 100 AGCCGGAATCTCAAAACATATCGTGGTCATATGATAACGACACTTTCGACGGTGGCG 159
QY 926 AAGGGGACGGGTACCCCTATAATTGATCGCGCAATGCGCAACTGCAACTCAAACTGGTT 985
Db 160 AGGCGGACAGGTTTCCAAATTTGGACGAGCTATGCGACAGATGAATACGATAGTT 219
QY 986 GGATGCAAAATCGCTTTAAGAAATGATTACTGCTCTTTTATAGTAAAAAATTTACACATCG 1045

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Db      220 ATATGCAACCGATCGCGATGATCGTCGCTTCATTTCTGGCAAGGACCTTTGTGG 279
Qy      1046 ATTGGCGTGGGTGAAAAATACITTCACAAAATGTTGATTGATGATGATGCTGCCAATA 1105
Db      280 ACTGGCAAAAGGAGAGAAATACITTTATGGAGCATCTCGTTGACGGGACCTTTGCCTCGA 339
Qy      1106 ATATCGGTGGCTGGCAATGGCTCTTCAACAGAACGGACGCTGTCCCTTATTTTCGGA 1165
Db      340 ACAACGGCGGTGGGTTTCAGTCTAGTGTGCGGTGCGACCTCAACCATACTTCCGTA 399
Qy      1166 TTTTATATCCAAATATCCAGTCAAAAAAATTTGATAATGACGGCAGTTCATCAAAAAAT 1225
Db      400 TTTTCAATCCTTGTCTACAGAGTGAGAGTTTGA-CCTGACGGGCAITACATCGCAAGT 458
Qy      1226 ATGTTCCAGAACTTAAGCAAGTGCACAAAAGTATATTCATCAACCAAAAT 1275
Db      459 GGGTTCCTGAGCTGAAGACCTTGACAATAAGGCGATTTCATGATCCGTAT 508

```

RESULT 9

CNS071TH/c
LOCUS clone BAOAB005C10 of library BAOAB from strain CLIB 210 of Kluveromyces lactis, genomic survey sequence.

AL425355
AL425355.1 GI:12208549

VERSION GSS.

KEYWORDS Kluveromyces lactis

SOURCE Kluveromyces lactis

ORGANISM Kluveromyces lactis

REFERENCE Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

AUTHORS Saccharomycetales; Saccharomycetaceae; Kluveromyces.

1 (bases 1 to 991)

2 (bases 1 to 991)

3 (bases 1 to 991)

4 (bases 1 to 991)

5 (bases 1 to 991)

6 (bases 1 to 991)

7 (bases 1 to 991)

8 (bases 1 to 991)

9 (bases 1 to 991)

10 (bases 1 to 991)

11 (bases 1 to 991)

12 (bases 1 to 991)

13 (bases 1 to 991)

14 (bases 1 to 991)

15 (bases 1 to 991)

16 (bases 1 to 991)

17 (bases 1 to 991)

18 (bases 1 to 991)

19 (bases 1 to 991)

20 (bases 1 to 991)

21 (bases 1 to 991)

22 (bases 1 to 991)

23 (bases 1 to 991)

24 (bases 1 to 991)

25 (bases 1 to 991)

26 (bases 1 to 991)

27 (bases 1 to 991)

28 (bases 1 to 991)

29 (bases 1 to 991)

30 (bases 1 to 991)

31 (bases 1 to 991)

32 (bases 1 to 991)

33 (bases 1 to 991)

34 (bases 1 to 991)

35 (bases 1 to 991)

36 (bases 1 to 991)

37 (bases 1 to 991)

38 (bases 1 to 991)

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41 (bases 1 to 991)

42 (bases 1 to 991)

43 (bases 1 to 991)

misc_feature
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/clone_lib="BAOAB"
complement (<391..>987)
/notes="similar to Saccharomyces cerevisiae ORF YOR386w [PHR1 ; deoxyribodipyrimidine photo-lyase]"
/evidence=not_experimental

ORIGIN

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Query Match      7.8%; Score 111.6; DB 11; Length 991;
Best Local Similarity 57.3%; Pred. No. 1.1e-16;
Matches 216; Conservative 2; Mismatches 158; Indels 1; Gaps 1;

Qy      881 ATATTCAATGCAAAATGACCCAGAAATGTTTGTCAAGTGGCAAAAGGGAGAC-GGGG 939
Db      849 ACATTAATGGGAAATGACGTTTCTTATTCGAAAAATGGTGTACGGTGAACCTGGTA 790
Qy      940 TACCTTATAATTGATCGCGCAATGCGACAACCTCAATCAAACTGTTGGATGCACAAATCGC 999
Db      789 TCCCCATTTGTTGATGCAATATGCTTAAATGTTGAAGACAGATATATCAACACAGA 730
Qy      1000 TTAAAGATGATTAATCTCCTCTTTTATTTAGTTTAAATTTTACATCGATGGCGTTGGGT 1059
Db      729 TCACGTATGATTTATGCGTCATTTCTTTGGCAAAAACTHACTTATTGATTCGCGCTGGGT 670
Qy      1060 GAAAAATACITTCAAAAAATGTTGATGACTATGATGCTGCCAATATATCGGTGGCTGG 1119
Db      669 GACGCGTGGTTCGTTAAACATTTTGTATCGACTACGATACAGCATCTAATGTAGAGGTGG 610
Qy      1120 CAATGGCTGCTTCAACAGCAAGCGAGCTGTCCCTTATTTTCGGATTTTAAATCCAATT 1179
Db      609 GGATTTTGGCGACCGGATTTGACTGCCAGCCCTATYTCAGAGTGTTAACATGAAG 550
Qy      1180 ATCCAGTCAAAAAAATTTGATTAATACGCGCAGTTTCATCAAAAAAATATGTTCCAGAACTT 1239
Db      549 TNACAGAGTGAGAAATATGACCCAGAGAAAGTTCATTAGACATTTGGCTTGAATAATGAT 490
Qy      1240 AGCAAGTCCCAAAA 1256
Db      489 GAGAATGATTCAGACAA 473

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RESULT 10

BZ563216
LOCUS pac2-164_4145.xl pac2-164 Pseudomonas aeruginosa genomic clone
DEFINITION pac2-164_4145, genomic survey sequence.

ACCESSION BZ563216

VERSION BZ563216.1 GI:27186625

KEYWORDS GSS.

SOURCE Pseudomonas aeruginosa

ORGANISM Pseudomonas aeruginosa

REFERENCE 1 (bases 1 to 1063)

AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,

TITLE Whole-Genome-Sequence variation among multiple isolates of

JOURNAL J. Bacteriol. (2002) In press

COMMENT Contact: Chris K. Raymond

Genome Center

University of Washington

Box 352145, Seattle, WA 98105-2145, USA

Tel: 2062216954

Fax: 2066857244

Email: craymond@u.washington.edu

Class: shotgun.

Location/Qualifiers

1..1063

/organism="Pseudomonas aeruginosa"

/mol_type="genomic DNA"

/strain="2-164"

FEATURES

source

1..1063

/organism="Pseudomonas aeruginosa"

/mol_type="genomic DNA"

/strain="2-164"

FEATURES

source

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/db_xref="taxon:287"
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/note="clinical isolate 2-164 Whole genomic shotgun
library."

ORIGIN
Query Match 7.5%; Score 108.2; DB 9; Length 1063;
Best Local Similarity 56.7%; Pred. No. 7.9e-16;
Matches 200; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

Qy 919 TGGCAAAAGGGAGACGGGTACCCCTATATTCGATCGCGCAATCGCACAACTGAATCAA 978
Db 217 TGGCAACAGGGGGCCGACCGGATACCGATCATCGACGGGAATGGCCAGTTCGCGC 276

Qy 979 ACTGTTGGATGCACAATCGCTTAAGAATGATTACTGCTCTTTTATTTAGTTAAATTTA 1038
Db 277 ACCGGCTGGATGCACAATCGCTCGGATGGTGGTAGCGATGTTCTCTCAGCAAGAACTG 336

Qy 1039 CACATCGATTGGCTGGGGTGAATAATATTTTCAAAAATGTTGATTGACTATGATGCT 1098
Db 337 CTGATCGACTGGCGGAAGGCGACGCTGTTTCATGCGCCACCTCATCGACGGTGACCTG 396

Qy 1099 GCCAATATATCGGTGGCTGGCAATGGCTGCTTCAACAGGAACGGAGCGCTGCTCCCTTAT 1158
Db 397 CGCGCAACACGGCGGCTGGCAGTGGAGCGGATCCACCGGACCGAGCGGTCCCTAC 456

Qy 1159 TTTCGGATTTTAAATCAATATTCAGTCAAAAAAATTTGATAATGACGGCCAGTTTCATC 1218
Db 457 TTCGCTGTTCAATCCGCTCTCGAGTCCGAACGCTTCGATCCACGGCGGAGTTTCATC 516

Qy 1219 AAAAAAATGTTCCAGAACTTAAGCAAGTGCACAAAAGTATATTCATCAACC 1271
Db 517 CGCCACTGGCTGCGGAACTGGCGCGCTGGAGCGCAAGGCGATCCACGATCC 569

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RESULT 11
LOCUS CL692005 773 bp DNA linear GSS 10-JUL-2004
DEFINITION PRI0157d G11.2 - PRI0157d.BR (773) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL692005
VERSION CL692005.1 GI:50213913
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 773)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBMED 14681447
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spananstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1. .773
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 7.5%; Score 107.6; DB 10; Length 773;
Best Local Similarity 62.8%; Pred. No. 1.1e-15;
Matches 167; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qy 1006 ATGATTACTGCTCTCTTTTGTAGTTAAAAATTTACACATCGATTGGCGTTGGGFTGAAAAA 1065
Db 2 ATTATTACAGCCAGTTTCTGTTTAAAGATTGTTGATGACTGGCGCAAGGCGAGCGA 61

Qy 1066 TACTTTCAAAAAATGTTGATTGATGCTGCTCCAAATATATATCGTGGCTGCGCAATGG 1125
Db 62 TATTTATGTCGCGAGCTGATTGATGTTGTTGCGACCAATAACCGTGGCTGGCAGTGG 121

Qy 1126 GCTGCTTCAACAGCAAGGAGCGCTGCTCTTATTTTCGGATTTTATCAATATATCCAG 1185
Db 122 GCCGCTTCAACCGGAACCGGATGCGAGCGCGGTATTTTCGTATTTTCAACCCGCAACCCAG 181

Qy 1186 TCAAAAAAATTTGATATATGACGCCAGTTTCATCAAAAAATATGTTCCAGAACTTTAAGCAA 1245
Db 182 GCGAGAAATTTGACCGTGAGGCGAGTTTATTCGTCGATGTTACCGAGCTGCGCAT 241

Qy 1246 GTGCCACAAAAGTATATTCATCAACC 1271
Db 242 GTACCAGGAAAGCGGTGCATGAGCC 267

RESULT 12
LOCUS BZ893625 420 bp DNA linear GSS 30-JUL-2003
DEFINITION HUS_0136 H1 pUC18 Library Halorubrum lacusprofundi genomic 5',
genomic survey sequence.
ACCESSION BZ893625
VERSION BZ893625.1 GI:33344215
KEYWORDS GSS.
SOURCE Halorubrum lacusprofundi
ORGANISM Halorubrum lacusprofundi
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halorubrum.
REFERENCE 1 (bases 1 to 420)
AUTHORS Goo,Y., Roach,J., Glusman,G., Baliga,N.S., Deutsch,K., Pan,M.,
DasSarma,S., Ng,W.V. and Hood,L.
TITLE Low-pass Sequencing for Microbial Comparative Genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Goo Y
Institute for Systems Biology
1441 North 34th Street, Seattle, WA 98103, USA
Tel: 206 732 1412
Fax: 206 732 1299
Email: ygoo@systemsbiology.org
Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1. .420
/organism="Halorubrum lacusprofundi"
/mol_type="genomic DNA"
/strain="ATCC 49239"
/db_xref="taxon:2247"
/clone_lib="H1 pUC18 Library"
/note="Vector: pUC18; Site 1: SmaI; A shotgun library was
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using pUC18/SmaI/BAP plasmid"

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ORIGIN
Query Match 7.4%; Score 106.8; DB 9; Length 420;
Best Local Similarity 59.6%; Pred. No. 1.5e-15;
Matches 180; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

Qy 889 TGGACAAATGACCCCAAAATGTTTCAAGTGGCAAAAAGGAGACGGGTACCTATA 948
Db 110 TGGCGGACGACCCCGACGAGATCGCGCGTGGAAAGCGTGGCGAGACGGGTACCCATC 169

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USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
Fax: 713-798-7078
Email: mgrusak@bcm.tmc.edu
B398204e
TIGR sequence name: MTPAS54TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA Gtg gat CC).

FEATURES

Location/Qualifiers
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/dev_stage="Immature seeds, 11 to 19 days after
pollination"
/clone_lib="GSD"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Immature seeds, collected from pods ranging in age
from 11 to 19 days after pollination, were harvested from
greenhouse-grown plants. Seeds were removed and
separated from pod walls and were immediately frozen in
liquid nitrogen. Seeds throughout the age range were
pooled for mRNA extraction. cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into
the Unizap XR vector from Stratagene and packaged using
GigaPack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-Zap
phage using Ex-assist helper phage and propagated in
XL10L cells."

ORIGIN

Query Match 7.3%; Score 104.6; DB 3; Length 748;
Best Local Similarity 50.9%; Pred. No. 5.9e-15;
Matches 248; Conservative 0; Mismatches 239; Indels 0; Gaps 0;
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Db 1 TTTTCTTGGATACCGATCTCTTCAAGTTAAGGCTTGAGGCTAGGTAGGACTGGATA 60
QY 942 CCTATAATTTGATGCGCAATGCGCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1001
Db 61 TCCATAGTTGATGCGCAATGCGGAGCTTTGGGCGACCGATGATGATGATGATGATGAT 120
QY 1002 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1061
Db 121 GCGAGTTATAGTTTCTAGTTTGTGAGTGAATGTTGCTTATACCATGGAATGGGAAT 180
QY 1062 AAAATCTTTCAAAAATGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1121
Db 181 GAAATATTTTGGGATACACTATTAGTGTGATGATGATGATGATGATGATGATGATGATG 240
QY 1122 ATGGGCTGCTTCAACAGGAACGACGCTGTCCCTTATTTTCGATTTTTCGATTTTTCGAT 1181
Db 241 GTATATCTCGGGAGCTTACCTGATGTTGATGATGATGATGATGATGATGATGATGATG 300
QY 1182 CCAGTCAAAAAATTTGTAATGACGGCGATTTTCAATCAAAAAATGATTTTCCAGAACTTAA 1241
Db 301 TCAAGGAGCAATACGATCCAGAGGCAATACATTCGACAAATGGCTACCGAGTTGGC 360
QY 1242 GCAGTGCACAAAGTATATTTCAATCAACCAATTAATGAAAGCAAGCTTCAACACGCA 1301
Db 361 AAGAAATTTCAACTGAGTGGATCCATCATTCATGGAATGCACCTACTGTGCTAAAGC 420
QY 1302 ATATCATGTATTTAGGAGAAATTTATCAAAACCCATTTGCTGATTTGATTCATCAAGTAA 1361
Db 421 ATCAGTATAGATTAGTCAAAACTATCCAAACCAATCATTTGAAATAGATTGGCTAG 480
QY 1362 AAAACAA 1368

Db 481 AGAACAA 487

RESULT 15

BQ854812 699 bp mRNA linear EST 14-AUG-2002
QGB24E15.yg.ab1 QG ABCDI lettuce salinas Lactuca sativa cDNA clone
LOCUS QGB24E15, mRNA sequence.
DEFINITION BQ854812
ACCESSION BQ854812
VERSION BQ854812.1 GI:22240277
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
REFERENCE 1 (bases 1 to 699)
AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
JOURNAL http://compgenomics.ucdavis.edu/
COMMENT Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmudson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
singleton, see http://cgdb.ucdavis.edu/ for details.
Plate: QGB24 row: E column: 15.

FEATURES

Location/Qualifiers
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/db_xref="taxon:4236"
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/lab_host="E.coli"
/clone_lib="QG ABCDI lettuce salinas"
/note="Vector: pBRCNDNA5fAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=leaves dark grow
TAG_LIB=QG ABCDI lettuce salinas
TAG_SEQ=GCTAGTCGGG"

ORIGIN

Query Match 7.2%; Score 103.6; DB 5; Length 699;
Best Local Similarity 50.8%; Pred. No. 1e-14;
Matches 247; Conservative 0; Mismatches 239; Indels 0; Gaps 0;
QY 787 TTCAAAAGAGATTAGCTTGGCGCACTTTTCAATATATCATCTATAGTGGTTCCACAA 846
Db 90 TTCTTAAATCAATTGGTTTTCGAAATATTCGCTTACATTTGTTTAAATTTCCATTC 149
QY 847 CAAAAGAGAGAGCTATTCAAGAAAAATTCGTTTATTTCAATGGCAAAATGACCAGAA 906
Db 150 ACTCAGAAAGATCGCTTTTAAATACTTAAAGTATTTCCCATGGCAAGCTAATGAAGCA 209
QY 907 ATGTTTGTCAAGTGGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
Db 210 CACTTTAAGGCTTGGAGACAGAGGTCGGACAGGCTACCGGTAGTTGATCGGGATGAGA 269

Qy	967	CAACTGAATCAAACTGGTTGGATCGACAAATCGCTTAAGAATGATTACTGCCTCTTTT	1026
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Qy	1027	GTTAAAAATTTACACATCGATTGGGTTGGGTTGAAAAATACTTTCAAAAAAATGTTGATT	1086
Db	330	GTCAGTGTTTTGTGTGCTTGGCAATGGGGGATGAAGTATTTTGGGATACGCTTTTG	389
Qy	1087	GACTATGATGCTGCCAAATAATCGTGGCTGGCAATGGGCTGCTTCAACAGGAACGGAC	1146
Db	390	GATCGGATCTTGAAGATGATGTTCTTGGTTGGCAGTATATCTGGGAGCTTGCCAGAT	449
Qy	1147	GCTGTCCCTTATTTTCGGATTTTAAATCCAATTATCCAGTCAAAAAAATTTGATAATGAC	1206
Db	450	GGGATGACCTTCGGCGCTTTGATAGCCCCGAGGTTCAAGGATTCAAATATGACCCCGAG	509
Qy	1207	GGCCAGTTTCATCAAAAAAATATGTTCCAGAACTTAAGCAAGTGCCACAAAAAGTATATT	1266
Db	510	GGTGAATACATAAGACAAATGGCTACCCGAATTATCAAGAAATACCAACCGAATGGATCCAT	569
Qy	1267	CAACCA	1272
Db	570	CATCCA	575

Search completed: December 20, 2005, 21:48:57
Job time : 6270 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using aw model

Run on: December 20, 2005, 16:59:36 ; Search time 296 Seconds

(without alignment)
8611.566 Million cell updates/sec

Title: US-10-758-979-2

Perfect score: 1434

Sequence: 1 atgaagaggaatattggtt.....acaatccaaaggtttcaataa 1434

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	942	65.7	966	3	US-09-134-000C-1312
2	597	41.6	609	3	US-09-134-000C-1313
3	212.2	14.8	1446	3	US-09-543-681A-4149
4	206.2	14.4	1393	3	US-08-956-171B-594
5	206.2	14.4	1393	3	US-08-781-986A-594
6	203.4	14.2	1608	3	US-09-328-352-389
7	201.4	14.0	5024	2	US-08-920-812-7
8	201.4	14.0	5024	2	US-08-920-827-7
9	201.4	14.0	5024	2	US-08-921-177-7
10	201.4	14.0	5024	2	US-08-362-577C-7
11	201.4	14.0	5024	2	US-08-920-828-7
12	199	13.9	1380	3	US-09-134-001C-2629
13	184.8	12.9	640681	3	US-09-790-988-1
14	137.2	9.6	1698	3	US-09-614-221A-226
15	117.4	8.2	1248	3	US-09-489-039A-6144
16	109.8	7.7	1638	3	US-09-252-991A-13995
17	109.8	7.7	2514	3	US-09-252-991A-14142
18	102.6	7.2	2200	2	US-08-272-255-21
19	102.6	7.2	2200	6	PCT-US95-08565-21
20	80	5.6	2458	2	US-08-272-255-5
21	80	5.6	2458	6	PCT-US95-08565-5
22	74	5.2	1977	2	US-08-272-255-17
23	74	5.2	1977	6	PCT-US95-08565-17
24	62.4	4.4	330	3	US-09-489-039A-5657

25	48.2	3.4	1141	3	US-09-806-708B-22	Sequence 22, Appl
26	47.2	3.3	1664976	3	US-08-916-421B-1	Sequence 1, Appl
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28	43.2	3.0	832	3	US-09-621-976-2813	Sequence 2813, Ap
29	42.4	3.0	1241	2	US-07-593-657-6	Sequence 6, Appl
30	42.4	3.0	1241	3	US-08-942-012B-3	Sequence 3, Appl
31	41.8	2.9	1141	3	US-09-806-708B-22	Sequence 22, Appl
32	40.6	2.8	492	3	US-09-270-767-6893	Sequence 6893, Ap
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34	40.6	2.8	601	3	US-09-949-016-185665	Sequence 185665,
35	40.6	2.8	113966	3	US-09-949-016-12727	Sequence 12727, A
36	40.6	2.8	113967	3	US-09-949-016-17051	Sequence 6, Appl
37	40.2	2.8	1710	3	US-09-618-425-6	Sequence 4, Appl
38	40.2	2.8	2450	3	US-09-618-425-4	Sequence 37, Appl
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40	40	2.8	1680	3	US-09-248-796A-4378	Sequence 6612, Ap
41	39.6	2.8	349	3	US-09-270-767-6612	Sequence 21894, A
42	39.6	2.8	349	3	US-09-270-767-21894	Sequence 5237, Ap
43	38.6	2.8	1782	3	US-09-248-796A-5237	Sequence 17195, A
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ALIGNMENTS

RESULT 1
US-09-134-000C-1312
; Sequence 1312, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1312
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1312

Query Match	65.7%	Score 942;	DB 3;	Length 966;
Best Local Similarity	99.9%	Pred. No. 2.3e-252;		
Matches 953;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
QY	1	ATGAAAAGAGTAATATGTTTACAGTGTATTTACGATTTACAGGATAATAAAGCATTTAGCA	60	
Db	13	ATGAAAAGAGTAATATGTTTACAGTGTATTTACGATTTACAGGATAATAAAGCATTTAGCA	72	
QY	61	CACGGTTTACAAAATCTTCGACGTGATGAATTTATTTATTTTCCAAATGAATCTCAA	120	
Db	73	CACGGTTTACAAAATCTTCGACGTGATGAATTTATTTATTTTCCAAATGAATCTCAA	132	
QY	121	CAATTTATTTCAAGAAAGTGCTAATCATAAACGCTTTTTTTTGCAGCTTAGCTCGTTCAAA	180	
Db	133	CAATTTATTTCAAGAAAGTGCTAATCATAAACGCTTTTTTTTGCAGCTTAGCTCGTTCAAA	192	
QY	181	GAACGAATGATCAAGAGGACATTTACAAATCATGTCGGCGACCATTTAGATTTATTT	240	
Db	193	GAACGAATGATCAAGAGGACATTTACAAATCATGTCGGCGACCATTTAGATTTATTT	252	
QY	241	TCACGTTTGAACGCAAAATTTACCGATTTGGCAGGCAATTTATTTTAAATGAAGATCTGT	300	
Db	253	TCACGTTTGAACGCAAAATTTACCGATTTGGCAGGCAATTTATTTTAAATGAAGATCTGT	312	
QY	301	GGCTTTGGGCGCAAGCGGACCAAGCAAGCTATCGCTTTTTTTTGAAGAAAATATATTCAG	360	

Db 313 GGCTTTGGGCAAGCGGACAGCAAGCTATGCGCTTTTGAAGAAAATAATATTCAG 372
Qy 361 TCTTTCCTTTTCAAGATGCTTATTTGATGGCTCTGAAGAAATTAAGAAGACGATGGC 420
Db 373 TCTTTCCTTTTCAAGATGCTTATTTGATGGCTCTGAAGAAATTAAGAAGACGATGGC 432
Qy 421 AGCAAGTACCAAGTGTCTTACGCCCTATTACAAATAAATGGAAGAGCGCCCTAAAGAAACA 480
Db 433 AGCAAGTACCAAGTGTCTTACGCCCTATTACAAATAAATGGAAGAGCGCCCTAAAGAAACA 492
Qy 481 CCGATTCTGTTTCTCTATACAGCTGAAAAAAATTTTAGTGGCTGTCTTTTCCAGAAGAG 540
Db 493 CCGATTCTGTTTCTCTATACAGCTGAAAAAAATTTTAGTGGCTGTCTTTTCCAGAAGAG 552
Qy 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAACACATATAGTGTGCGGAA 600
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Qy 601 GAAACAGCCAGAGCGCTTAAATACCTTTTATGATCAAAAATTCATCTCTATGAATAAT 660
Db 613 GAAACAGCCAGAGCGCTTAAATACCTTTTATGATCAAAAATTCATCTCTATGAATAAT 672
Qy 661 AAGCGTGATTTTCTTATCAGGATCAACGAGTCTGTCTACTTTTTTAAGAACGGGA 720
Db 673 AAGCGTGATTTTCTTATCAGGATCAACGAGTCTGTCTACTTTTTTAAGAACGGGA 732
Qy 721 GAACTTCGATTCGACCATTTGGGAAGAGCTTGATCTGTGCTCTCTAGCTTAAGTAAA 780
Db 733 GAACTTCGATTCGACCATTTGGGAAGAGCTTGATCTGTGCTCTCTAGCTTAAGTAAA 792
Qy 781 GAAACCTTCAAAAAGAAATAGCTTGGCGGACTTTTACAAATATGATCTATAGTGGCTTT 840
Db 793 GAAACCTTCAAAAAGAAATAGCTTGGCGGACTTTTACAAATATGATCTATAGTGGCTTT 852
Qy 841 CCACAAACAAAGAGGAGCTATTCAAGAAAAATTTTCGTATATTCAATGACAAATGAC 900
Db 853 CCACAAACAAAGAGGAGCTATTCAAGAAAAATTTTCGTATATTCAATGACAAATGAC 912
Qy 901 CCAGAAATGTTTCAAGTGGCAAAAAGGGAGAC-GGGGTACCTATATTTGA 953
Db 913 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGAGACGGGGGTACCTATATTTGA 966

RESULT 2
US-09-134-000C-1313
; Sequence 1313, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1313
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1313

Query Match 41.6%; Score 597; DB 3; Length 609;
Best Local Similarity 99.8%; Pred. No. 2.6e-156;
Matches 608; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 827 TCTATAGTGGCTTTCCACAAACAAAGAGGAGCTATTCAAGAAAAATTTTCGTATATTC 886
Db 1 TCTATAGTGGCTTTCCACAAACAAAGAGGAGCTATTCAAGAAAAATTTTCGTATATTC 60
Qy 887 AATGACAAATGACCCAGAAATGTTTGTCAAGTGGCAAAAAGGGAGAC-GGGGTACCT 945

Db 61 AATGGCAAAATGATCCCAAGAAATGTTTGTCAAGTGGCAAAAAGGGAGACGGGGTACCT 120
Qy 946 ATAATTGATCGCGCAATGCGACAACTGAATCAAACTGGTGGATGCACAATCGCTTAA 1005
Db 121 ATAATTGATCGCGCAATGCGACAACTGAATCAAACTGGTGGATGCACAATCGCTTAA 180
Qy 1006 ATGATTACTCGCTCTTTTGTAGTTAAAAATTTACACATCGATTGGCGGTGGGGTGA 1065
Db 181 ATGATTACTCGCTCTTTTGTAGTTAAAAATTTACACATCGATTGGCGGTGGGGTGA 240
Qy 1066 TACTTTCAAAAAATGTTGATTGACTGCTGCCAATAATATCGGTGGCTGGCAATGG 1125
Db 241 TACTTTCAAAAAATGTTGATTGACTGCTGCCAATAATATCGGTGGCTGGCAATGG 300
Qy 1126 GCTGCTTCAACAGAACGCGCTGCTCTTATTTTCGGATTTTTCGCAATATATCCAG 1185
Db 301 GCTGCTTCAACAGAACGCGCTGCTCTTATTTTCGGATTTTTCGCAATATATCCAG 360
Qy 1186 TCAAAAAATTTGATATGACGCGCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAA 1245
Db 361 TCAAAAAATTTGATATGACGCGCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAA 420
Qy 1246 GTGCCACAAAAGTATATTCATCAACCAAAATCTAATGAACGAAGCTTTACAAACGCAATAT 1305
Db 421 GTGCCACAAAAGTATATTCATCAACCAAAATCTAATGAACGAAGCTTTACAAACGCAATAT 480
Qy 1306 CATGTACATTTAGAGAAAAATTTACAAAACCCATTTGTCGATTTATGATCAAGTAA 1365
Db 481 CATGTACATTTAGAGAAAAATTTACAAAACCCATTTGTCGATTTATGATCAAGTAA 540
Qy 1366 CAAACATTTGTTCTATATGAGCGCAGCAAGAAATTCATCAAGAAATGAACAATCC 1425
Db 541 CAAACATTTGTTCTATATGAGCGCAGCAAGAAATTCATCAAGAAATGAACAATCC 600
Qy 1426 TTTCAATAA 1434
Db 601 TTTCAATAA 609

RESULT 3
US-09-543-681A-4149
; Sequence 4149, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4149
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-4149

Query Match 14.8%; Score 212.2; DB 3; Length 1446;
Best Local Similarity 60.0%; Pred. No. 6.9e-49;
Matches 418; Conservative 0; Mismatches 258; Indels 21; Gaps 3;
Qy 596 GCGAAGAAACAGCCAGAGCGCTTAAATACTTTTATGATCAAAAACTTCAATCTATG 655
Db 635 GCGAAGAAACAGCCAGCGCTTAAACACAGTTTTCGTATGAAAGGGTGATACATTATG 694
Qy 656 AAATAAGCGGTGATTTTCCTTATCAGATCAAGAGTCATCTCTACTCTTTTAAAGAA 715
Db 695 CAAAATGGCGAGATATTCCTGCTATTGATGGAACCAAGTCAATATCCCTTATCTGCCA 754
Qy 716 CGGAGAAACTTTCGATTGCGACCATTTTGGCAAGAGCTTGC---ATCTGTGCTTCTAGCT 772

Db 755 TAGGCTAGTCTCTGCGCCCAATGTTTAAATCGCTTTTACAAACAGAGCCTGATTTCT 814
Qy 773 TAAGTAAAGAAACCTTCAA-----AAAGATTAGCTTGGCGCCACTTTT 817
Db 815 TAGAAAATAACCAATTCAGAGTGCATTTGTTGGTTTAAATGAGTTAGTTTGGCGCGAGTTT 874
Qy 818 ---ACATATGATCTATAGTGGTTTCCACAAACAAAGAGAGAGCTATTCAAGAAAAT 874
Db 875 ATCAACATCTAATAGTTGCTAACCGGAGTTTATCCAAACAGATAGCTTTCAACCATGGA 934
Qy 875 TTGCTTATTTCAATGGCAAAATACCCAGCAAAATGTTTGTCAAGTGGCAAAAGGGGAGA 934
Db 935 CAGAAAATATTCGCTGGCGTAAAGCAAACTGAATTTACCGCTTGGACACAGGCTTAA 994
Qy 935 CGGGTACCTTATTAATGATCGCGCAATGGACAACTGAATCAAACTGGTTGGATGCACA 994
Db 995 CAGGCTTTCCTATTATTATGATCGCGGATGCGACAACTGAATCAAAACCGGCTGSGATGCACA 1054
Qy 995 ATCGCTTAAGATGATTACTGCTCTTTTGTAGTTTAAATAATTTACACATCGATTGGCGTT 1054
Db 1055 ATCGCTTACGTAATGCTGACGGCAAGTTTATTTAGTCAAAAGATCTATTAATGATGGCGCT 1114
Qy 1055 GGGGTGAAAAATACCTTCAAAAAATGTTGATTGACTATGATGCTGCCAATTAATATCGGTG 1114
Db 1115 GGGGGAAATATTTATGTCACAAATTAATGATGGTGAATTCGCGTCAAAATATGCTG 1174
Qy 1115 GCTGCAATGGCTGCTTCAACAGAAACGGAGCTGTCCTTATTTTCGGATTTTAAATC 1174
Db 1175 GCTGCAATGGCTGCTCAACAGGCACTGATGCTGCTTATTTTCGTATTTTAAATC 1234
Qy 1175 CAATTATCGAGTCAAAAAATTTGATAATGACGGCCAGTTTCATCAAAAAATGTTCCAG 1234
Db 1235 CGACAACCCAGGACGTAAGTTTGAATCTGATGCTGATGTTATCCGCACTGGCTACCAG 1294
Qy 1235 AACTTAAGCAAGTGGCACAAAAAGTATATTTCATCAACC 1271
Db 1295 AGCTTGCTGATGCCAGATGCTATATCCATACTCC 1331

RESULT 4

US-08-956-171E-594
; Sequence 594, Application US/08956171E
; Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 594:
SEQUENCE CHARACTERISTICS:
LENGTH: 1393 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 594:
US-08-956-171E-594

Query Match 14.4%; Score 206.2; DB 3; Length 1393;
Best Local Similarity 56.2%; Pred. No. 3.2e-47;
Matches 432; Conservative 0; Mismatches 328; Indels 9; Gaps 2;

Qy 627 TTTTATTGATCAAAAACTTCAATCCCTATGAAAAATAGCGTGAATTTCTTTATCAGATCA 686
Db 617 TTTTATTGATCAAGATATACAGAAATTACGAAGCGGAGAGACTATTTACTGAATTT 676
Qy 687 AACGAGTCACTCTCTACTTTTTTAAAGAACGGAGAACTTTTCGATTCGCACCAATTTGGCA 746
Db 677 AACAGTCACTAAGTGTCTTTTAGCATATGATTTAGATATATTAGAAATTTTAA 736
Qy 747 AGA-----GCTTGCATCTGTGCTTCTAGCTTTAAGTAAAGAAACCTTCAAAAAAGATT 800
Db 737 TGATTTATTGCGCGTTATGATGAAGATGAGGCAAACTATGAAGCATTTTATCGTGAAT 796
Qy 801 AGCTTGGCGGACTTTTACAAATGATGCTATAGTGGCTTTCCACACAAAAAGAGGAGC 860
Db 797 CATTTTATAGAGATTTTATTATGTTAATGACACAGTATCTTGAACCTCATACCAAGC 856
Qy 861 TATTCAAGAAAAATTTTCGTTATATTCAATGGACAAATGACCCAGAAATGTTTGTCAAGTG 920
Db 857 TTTCAAACTAATATCGACAGATAAATGTCGCAAAATGAAGCGATTTTAAATGATG 916
Qy 921 GCAAAAAAGGAGACAGGGGTACCTATAATATGATGCGCGAATGGCAACATGATCAAC 980
Db 917 GTGCAAGGCAACACAGGATTTCCAATCATTTGATGACAGCAATATGGAATTTGACACAAAC 976
Qy 981 TGGTTGATGCACAAATCGCTTAAAGATGATTACTGCTCTTTTGTAGTAAATAATTTTACA 1040
Db 977 TGGTTTATGCTAATCAATGGAATGCTGTCGCAATTTTAAACCAAGATTTATT 1036
Qy 1041 CATCGATTGGGCTTGGGTTGAAAAATACTTTCAAAAAATGTTGATTTGACTATGCTGC 1100
Db 1037 TATGATTTGACATGGGAGAAAAATTTCTTTAGAAAGCACCTTATTGACTATGATGACG 1096
Qy 1101 CAATAATATCGTGGCTGGCAATGGGCTGCTTCAACAGGAACGGACGCTGTCCTTATT 1160
Db 1097 ATCAATATTTCATGATGGCAATGCTGCTTCTACAGGTACGGATGCGTGGCTATT 1156
Qy 1161 TCGGATTTTAAATCCAAATTTCCAGTCAAAAAATTTGATAATGACCGCCAGTTTCATCA 1220
Db 1157 TAGAATGTTTAAATCCAAATGAACAGAGTGAACGCTTTGATGCTAAAGCTTTGTATATCA 1216
Qy 1221 AAAATATGTTCCAGAACTTAAAGCAAGTGCACAAAAAGTATATTTCATCAACCAATCTAAT 1280
Db 1217 AACATATCTCCGATTTTAAATCAAAATGATGCAAAATATTTCATGATGATACA---CAACG 1273
Qy 1281 GAACGAAGCCTTCAAAACGGCAATATCATGTACATTTTAGGAGAAAATTTATCAAAACCCAT 1340
Db 1274 CAATGATGCCAACCTTTTGAACAGGGGATGGAATTAGGTAGTCAATTATCAAGACAAAT 1333
Qy 1341 TGTGATTTGATCAAGTAAATAAAAAACAACTTTGTTTCTATATGAAGC 1389
Db 1334 GGTAGATCATCAAGAAAAACGTACACAAAGTTTGTAGCTACATTTTAAAGCG 1382

```

RESULT 5
US-08-781-986A-594
; Sequence 594, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781.986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 594:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1393 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-594

Query Match          14.4%   Score 206.2;   DB 3;   Length 1393;
Best Local Similarity 56.2%;   Pred No. 3.2e-47;
Matches 432;   Conservative 0;   Mismatches 328;   Indels 9;   Gaps 2;

Qy 627 TTTTATTGATCAAAACTTCAATCCTATGAAAAATAAGCGTGATTTTCCTTATCAGGATCA 686
      |||||
Db 617 TTTTATTGATCAAGATATACAGAAATTCGAAAGCGGAAGAGACTATTTTACTGTGAAGTATT 676

Qy 687 AACGAGTCATCTGCTACTTTTAAAGACGGGAGAACTTTGAGTTGCGACCACTTTGGCA 746
      |||||
Db 677 AACAGTCAGCTAAGTGTGCTTTAGCATATGGAATTTAGATATTGAAATTTTTTAA 736

Qy 747 AGA-----GCTTGCACTCTGCGCTTCTAGCTTAAGTAAAGAAACCTTCAAAAAAGAAATT 800
      |||||
Db 737 TGATTTATTGGCGGTTTATGATGAGATGAGGCAACTATGAGCACTTTATACGTGAAT 796

Qy 801 AGCTTGCGCGACTTTTACAATATGATCTATAGTCGCTTTTCCACAAACAAAAGAGGAAGC 860
      |||||
Db 797 CATTTTATAGAGAATTTTATTATGTTGTTAAATGACACAGACTATCCTGAAACCTCATACCAAGC 856

Qy 861 TATTCAAGAAAAATTCGTTTATATTCAATGGAACAAATGACCCGAAATGTTTGTCAAGTG 920
      |||||
Db 857 TTTCAAAACCTAAATATCGACAGATAAAATGTCGCAAAATGAAAGCGGATTTTAAATGCATG 916

Qy 921 GCAAAAAGGGAGACGGGGTACCTATAATTGATGCCGCAATGCGACAACTGAATCAAAC 980
      |||||
Db 917 GTGCAAGGCAACACAGATTTCAATCATTTGATGACGCAATTAATGGAATTGACACAAC 976

Qy 981 TGGTTGGATGCACAACTCGCTTTAAGAAATGATTACTGCTCTTTTTTACTTAAAAATTTACA 1040
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Qy 930 GGAGACGGGTACCTTAATGATCGCGCAACTGAATCAAACTGGTGGAT 989
Db 1167 TCAACCGGTATCTTATGTTGATGCTGGGATGGGCAACTTTTACAAACAGCGTGGAT 1226
Qy 990 GCACAATCGCTTAAGAATGATCTGCTCTTTTGTAGTTAAATTTACACATCGATTG 1049
Db 1227 GCATAATCGATGACGTATGATACAGCCATGTTTTATGTAAATAATCTTTTGAATTGATTG 1286
Qy 1050 GGTGTGGGGTGAATAATCTTCAAAAAATGTTGATGACATGATGCTGCCAATAATAT 1109
Db 1287 GCGCAATGTTGTAACAATGTTTATGCGACATTTAATGATGGTGACCTCGCGGCAATATA 1346
Qy 1110 CGGTGCTGGCAATGGGCTGCTTCAACAGGAACGAGCGCTGCTCCCTTATTTTCGGAATTT 1169
Db 1347 TGGCGGTTGGCATGTTGCTGCTCAACAGGACAGATGCGGTACCTTATTTTCGGAATTT 1406
Qy 1170 TAATCAATATTCCAGTCAAAAAATTTGATAATGACGGCGAGTTTCATCAAAAAATATGT 1229
Db 1407 CAACCAATTTGCTCAATCAAGAAGTTTGTATCCGGAGGAGAAATATATTCGCCAATGGGT 1466
Qy 1230 TCCAGAACTTAAGCAAGTCCCAAAAGTATATTCATCAACCAATCTAATGAACGAGC 1289
Db 1467 GAAAGATTGGCTCATTTTGGCAATTAATAACGAATTCATGAACCTTACTCAAGCAAAACCGA 1526
Qy 1290 CTTACAAACGCAATATGATGATATTTAGGAGAAATTTATCAAAACCAATTTGTCGATTA 1349
Db 1527 TCTTGGTTAAATTTCAAAACCATAGTAAATTTAAAGAAACACGCTTAAAGCAAT 1586
Qy 1350 TGCATCAAGTAAAAA 1364
Db 1587 TGAACCTTCAAGAA 1601

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RESULT 7

```

US-08-920-812-7
; Sequence 7, Application US/08920812
; Patent No. 5763188
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,812
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Lauree, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 5024 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-32
; US-08-920-812-7

Query Match      14.08; Score 201.4; DB 2; Length 5024;
Best Local Similarity 58.78; Pred. No. 1.2e-45;
Matches 368; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

Qy 774 AAGTAAAGAAACCTTCAAAAAAGAAATAGCTTGGCGCGACTTTTACAAATATGATCTATAG 833
Db 3624 AAATTAGCAAACTTTTATACGTGAATTTATTTTAGAGAGTTTATTTATGATTTAATGAC 3683
Qy 834 TGGCTTTTCCACACAAAGAGAGAGCTATTTCAAGAAAAATTTTGGTTATATTTCAATGAC 893
Db 3684 CAATTATCCCGAAACAGCTCATGTGCTTTTAAAGAAAAATACCAAAATTTGAAATGGTC 3743
Qy 894 AATGACCCAGAAATGTTTCAAGTGCAGAAAGGAGACGGGTACCCCTATAATTTGA 953
Db 3744 TTATAATGAAGAGAAATTTTAACTGTGGAAGATGGGAATACTGTTTCCAAATTTGA 3803
Qy 954 TGGCGCAATCGCAACACTGAATCAAACTGGTTGGATGCAACAATCGCTTAAAGAAATGATTAC 1013
Db 3804 TGCAGCAATGGAGGAACTTAAACAACTGGATTTATGCAATAATCGCATGAGATGGTAGT 3863
Qy 1014 TGCCTCTTTTGTAAAAATTTACACATCGATGGGTTGGGTTGAAAAATACTTTCA 1073
Db 3864 TTCTCAATTTTAACTAAAGATTTGTTTATTTGACTGGATTTGGGGTGGAGTCATTTTCAA 3923
Qy 1074 AAAAATGTTGATGATGATGCTGCAATTAATATCGTGGCTGGCAATGGGCTGCTTC 1133
Db 3924 ACAAAAATTAATAGATATGATGCACTTCAAAATGTTTCAAGATGGGAGTGGTCACTTC 3983
Qy 1134 AACAGGAACGACGCTGCTCCCTTATTTTTCGGATTTTAAATCCAAATTTATCCAGTCAAAAA 1193
Db 3984 TACTGGAAACAGATGCTGTACCATCTTTAGAAATGTTTAAATCTTAAAGCAAAAGCAGCG 4043
Qy 1194 ATTTGATAATGACGGCCAGTTTCATCAAAAAATATGTTTCCAGAACTTAAAGCAAGTGCACA 1253
Db 4044 TTTTGATAATAATGCACGATATATAAAAACTTACATTTCCAAAGATTTAAATCAGTAGATGC 4103
Qy 1254 AAAGTATATTTCATCAACCAATCTTAAGTGAACGAGCTTTACAAACGCAATATCATGTACA 1313
Db 4104 TAAGTATTTACACGATACTCATAAATTCGAGCAACAAATAAAGGGGCAAA---GGTGTGA 4160
Qy 1314 TTTAGGAGAAATTTATCAAAACCCATTTGCTGATTATGCAATCAAGTAAAAAACAAACATT 1373
Db 4161 AATAGGTAAGACATCTCTTAAACAAATGATTGATCACAAGAAAGTAGACAAACGTTGTAAT 4220
Qy 1374 GTTCTATATGAAGCGAGCAAGAAAT 1400
Db 4221 GTCAGAAATTCAGAGCTATAGATTAAAT 4247

```

RESULT 8

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US-08-920-827-7
; Sequence 7, Application US/08920827
; Patent No. 5770375
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

```



```
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,827
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5024 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-32
US-08-920-827-7

Query Match 14.0%; Score 201.4; DB 2; Length 5024;
Best Local Similarity 58.7%; Pred. No. 1.2e-45;
Matches 368; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

QY 774 AAGTAAAGAAACCTTCAAAAAGATTAGCTTGGCGGACATTTTACAAATATGATCTATAG 833
DB 3624 AAATTACGAACCTTTATACGTGAATGATTTTAGAGAGTTTATATGATTAATGAC 3683
QY 834 TGCCTTTCCACAAACAAAGAGGAGCTATTCAAGAAAAATTCGTTATATTCATGAC 893
DB 3684 CAATTATCCGAAACAGCTCATGTTGCTTTTAAAGAAAAATACCAACAATTGAAATGGTC 3743
QY 894 AAATGACCCAGAAATGTTTGTCAAGTGCRAAAGGGGAGCGGTACCTATAATTGA 953
DB 3744 TTATAATGAAGAGAAATTTTAAACTGTGGAAGATGGGAATACTGTTTCCAAATTATGA 3803
QY 954 TGCGCAATGCGACAACTGAATCAAACTGGTTGGATGCACAACTCGCTTAAGAAATGATTAC 1013
DB 3804 TGCAGCAATGAGGAACCTTAAACAACTGGATTTATGCAATATCGATGAGATGGTAGT 3863
QY 1014 TGCCTCTTTTATGTTAAATAATTTACACATCGATTGGCGTTGGGGTGAATAACTTTCA 1073
DB 3864 TTCTCAATTTTAACTAAAGATTTGTTTATTGACTGGATTGGGGTGAATCTTTTCAA 3923
QY 1074 AAAAATGTTGATTGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGTGCTTC 1133
DB 3924 ACAAAAAATTAATAGATATGATGACGCTTCAAAATGTTTCACGGATGGCAGTGGTCAGCTTC 3983
QY 1134 AACAGGAACGACGCTGTCCTTTATTTTCGATTTTAAATCCAATTTTCCAGTCAAAAAA 1193
DB 3984 TACTGGAAACAGATGCTGTGACCACTACTTTAGAAATGTTTAACTCTATAGACAAACGAGCG 4043
QY 1194 ATTTGATAATGACGGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCCACA 1253
DB 4044 TTTTGATAAATATGCACGATATATAAAAACTTACATTCGAAGATTAAATCAGGTAGATGC 4103
QY 1254 AAGTATATTTCATCAACCAAAATCTAATGAACGAAGCCCTTACAAACGCAATATCATGTACA 1313
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DB 4104 TAAGTATTTACACGATACATAAAATTCGAGCAACAATAAAGGGGCAA---GGTGTGA 4160
QY 1314 TTTAGAGAAAAATTCAAAAACCCATTTGTGATTTATGATCAAGTAAAAAACAACATTT 1373
DB 4161 AATAGGTAAGACTATCTCTAAACAAATGATTGATCAAAAGAAAGTAGACAACGTTGTAAT 4220
QY 1374 GTTCTTATATGAAGCGAGCAAGAAAT 1400
DB 4221 GTCAGAAATCAAAAGCTATAGATTAAAT 4247

RESULT 9
US-08-921-177-7
; Sequence 7, Application US/08921177
; Patent No. 5798211
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921,177
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5024 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-32
US-08-921-177-7

Query Match 14.0%; Score 201.4; DB 2; Length 5024;
Best Local Similarity 58.7%; Pred. No. 1.2e-45;
Matches 368; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

QY 774 AAGTAAAGAAACCTTCAAAAAGATTAGCTTGGCGGACATTTTACAAATATGATCTATAG 833
DB 3624 AAATTACGAACCTTTTATAGCTGAATGATTTTAGAGAGTTTATATGATTAATGAC 3683
QY 834 TGCCTTTCCACAAACAAAGAGGAGGAGCTATTCAAGAAAAATTCGTTATATTCATGAC 893
DB 3684 CAATTATCCGAAACAGCTCATGTTGCTTTTAAAGAAAAATACCAACAATTGAAATGGTC 3743
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894 AAATGACCCAGAAATGTTTGTCAAGTGCNAAAGGGGAGCGGTACCCCTATAATTGA 953
3744 TTATAAAGAGAGAAATTTTAAACTGTGGAAGATGGGAATACCTGGTTTCCAAATTAITGA 3803
954 TGCCGCAATCGACAACTGAATCAAACTGGTTGGATGCACAACTCCCTTAAGAATGATTAC 1013
3804 TCGACGATGGAGAACTTAAACAACTGGATTATGATATCCATCCATGAGATGGTAGT 3863
1014 TGCCTCTTTTATGTTTAAATTTTACATCATGATTTGGGTTGGGTTGGAATTAATTTTCA 1073
3864 TTCTCAATTTTAACTAAAGATTTGTTTATGACTGGAATTTGGGTTGGTCAATTTTCAA 3923
1074 AAAATGTTGATGACTATGCTGCGCAATTAATCGTGGCTGGCAATGGCTGCTTC 1133
3924 ACANAAATTAATAGATTAATGATGCAGCTTCAAAATGTTACGGATGGCAGTGGTCACTTC 3983
1134 AACAGNACGGAGCGTGTCCCTTATTTTCGATTTTAACTCCAAATTAATCCAGTCAAAAA 1193
3984 TACTGGAACAGATGCTGTACCATACTTTAGATGTTTAACTTAAAGCAAGCGAGCG 4043
1194 ATTGATTAATGACGGCAGTTTCAATCAAAAAATATGTTCCAGAACTTTAAGCAAGTCCACA 1253
4044 TTTTGATATAATGACGAGATATATAAAACTTTACATTTCCAGATTTAAATCAGGTAGATGC 4103
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1314 TTTAGAGAAATTAATCCAAACCCATTCGATTAATGATCAATCAAGTAAACAAACATTT 1373
4161 AATAGTAAAGACTATCTCTTAACAATGATGATCAAAAGAAAGTAGACAACTGTAAT 4220
1374 GTTCTTATATGAAGGAGCAAAAGAAAT 1400
4221 GTCAGAAATCAAGCTATAGATTAAAT 4247

RESULT 10
US-08-362-577C-7
; Sequence 7, Application US/08362577C
; Patent No. 5807673
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,577C
; FILING DATE: 27-MAR-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Heien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5024 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-32
; US-08-362-577C-7

Query Match 14.0%; Score 201.4; DB 2; Length 5024;
Best Local Similarity 58.7%; Pred. No. 1.2e-45;
Matches 368; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

QY 774 AAGTAAAGAAACCTTCAAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCATAG 833
DB 3624 AAATTACGAACTTTTATACGTGAATTTATTTAGAGAGTTTATTTATGTTATTAATGAC 3683
QY 834 TGCCTGTTCCACAAACAAAAAGAGAAAGCTATTCAAGAAAAATTTTCGTTATATTTCAATGGAC 893
DB 3684 CAATTATCCCGAAACAGCTCATGTTGCTTTTAAAGAAAAATACCAACAAATTTGAATGGTC 3743
QY 894 AAATGACCCAGAAATGTTTGTCAAGTGCNAAAGGGGAGCGGTACCCCTATAATTGA 953
DB 3744 TTATAAAGAGAGAAATTTTAAACTGTGGAAGATGGGAATACCTGGTTTCCAAATTAITGA 3803
QY 954 TGCCGCAATCGCACTGAATCAAACTGGTTGGATGCACAACTCCCTTAAGAATGATTAC 1013
DB 3804 TCGACGATGGAGAACTTAAACAACTGGATTATGATATCCATCCATGAGATGGTAGT 3863
QY 1014 TGCCTCTTTTATGTTTAAATTTTACATCATGATTTGGGTTGGGTTGGAATTAATTTTCA 1073
DB 1074 AAAATGTTGATGACTATGCTGCGCAATTAATCGTGGCTGGCAATGGCTGCTTC 1133
QY 1134 AACAGNACGGAGCGTGTCCCTTATTTTCGATTTTAACTCCAAATTAATCCAGTCAAAAA 1193
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QY 1254 AAAGTATATTATCAACCAATTAATGAACGAGCTTACAAACGCAATATCATGTACA 1253
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DB 1374 GTTCTTATATGAAGGAGCAAAAGAAAT 1400
QY 1400 GTTCTTATATGAAGGAGCAAAAGAAAT 1400
DB 4221 GTCAGAAATCAAGCTATAGATTAAAT 4247

RESULT 11
US-08-920-828-7
; Sequence 7, Application US/08920828
; Patent No. 5853998
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
Prior APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5024 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus epidermidis
STRAIN: Clinical Isolate SE-32
US-08-920-828-7

Query Match 14.0%; Score 201.4; DB 2; Length 5024;
Best Local Similarity 58.7%; Pred. No. 1.2e-45;
Matches 368; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

QY 774 AAGTAAGAAACCTTCAAAAAGAAAGTAGCTTGGCGGAGCTTTTACAAATATGATCTATAG 833
DB 3624 AAATTTACGAACTTTTATACGTGAATGATTTTAGAGAGTTTATTATGATTAATGAC 3683

QY 834 TCGCTTTCCACAAACAAAAGAGGAGCTATTCAAGAAAAATTTTCGTTATATTCATGGAC 893
DB 3684 CAATTTATCCGAACAGCTCATGTTGCTTTTAAAGAAATATACCAAAATGAAATGGTC 3743

QY 894 AAATGACCCAGAAATGTTTGTCAAGTGGCAAAAAGGGAGACGGGGTACCCTATAATGA 953
DB 3744 TTATAATGAAGAGAAATTTAAACTGTGGAAGATGGGAATACTGGTTTCCAAATTAATGA 3803

QY 954 TCGCGCAATGGCAACACTGAATCAACTGGTGTGATGCACAACTGCTTAGAATGATTAC 1013
DB 3804 TGCAGCAATGAGGAACCTTAAACAACTGGGATTTATGCATAACTCGCATGAGATGGTAGT 3863

QY 1014 TGCCTCTTTTGTAGTTAAATTTTACACATCGATTGGCGTTGGGGTGAAAAATACTTTCA 1073
DB 3864 TTCTCAATTTTAACTAAAGATTTGTTTATTTGACTGGATTTGGGGTGAGTCATTTTCAA 3923

QY 1074 AAAAATGTTGATGATATGATGCTGCGCAATAATATATCGGTGGCTGGCAATGGGCTGCTTC 1133
DB 3924 ACAAAAATTAATAGATTAATGATGACGCTTCAAAATGTTTCAACGATGGCAGTGGTCA 3983

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QY 1374 GTTCTATATATGAAGCGAGCAAGAAAT 1400
DB 4221 GTCAGAAATTCAAAAGCTATAGATTAAAT 4247

RESULT 12

US-09-134-001C-2629
; Sequence 2629, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; TELECOMMUNICATION INFORMATION:
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2629
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2629

Query Match 13.9%; Score 199; DB 3; Length 1380;
Best Local Similarity 58.9%; Pred. No. 3.2e-45;
Matches 362; Conservative 0; Mismatches 250; Indels 3; Gaps 1;

QY 774 AAGTAAGAAACCTTCAAAAAGAAATAGCTTGGCGGAGCTTTTACAAATATGATCTATAG 833
DB 759 AAATTTACGAACTTTTATACGTGAATGATTTTAGAGAGTTTATTATGATTAATGAC 818

QY 834 TCGCTTTCCACAAACAAAAGAGGAGCTATTCAAGAAAAATTTTCGTTATATTCATGGAC 893
DB 819 CAATTTATCCGAAACAGCTCATGTTGCTTTTAAAGAAAAATACCAAAATGAAATGGTC 878

QY 894 AAATGACCCAGAAATGTTTGTCAAGTGGCAAAAAGGGAGACGGGGTACCCTATAATGA 953
DB 879 TTATAATGAAGAGAAATTTAAACTGTGGAAGATGGGAATACTGGTTTCCAAATTAATGA 938

QY 954 TCGCGCAATGGCAACACTGAATCAAACTGGTGTGATGCACAACTGCTTTAAGAAATGATTAC 1013
DB 939 TGCAGCAATGAGGAGAACTTAAACAACTGGATTTATGCAATAATCGCATGAGATGGTAGT 998

QY 1014 TGCCTCTTTTGTAGTTAAATTTTACACATCGATTGGCGTTGGGGTGAAAAATACTTTCA 1073
DB 999 TTCTCAATTTTAACTAAAGATTTGTTTATTTGACTGGATTTGGGGTGAGTCATTTTCAA 1058

QY 1074 AAAAATGTTGATGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTC 1133
DB 1059 AAAAAATTAATAGATTAATGATGACGCTTCAAAATGTTTACGGATGGCAGTGGTCA 1118

QY 1134 AACAGGACGACGCTGTCCTTTATTTTCGATTTTAAATCAATATTCAGTCAAAAAA 1193
DB 1119 TACTGGAACAGATGCTGTACCATCTTTAGAATGTTTAACTCTATAAGA CAAAGCGAGCG 1178

QY 1194 ATTTGATATGACGGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAAGCAAGTGCCACA 1253
DB 1179 TTTTGATTAATGACGAGATATATAAAAACTTACATTTCCAAAGATTAATCAGGTAGATGC 1238

QY 1254 AAAGTATATTTTCATCAACCAAAATCTAATGAACGAAGCCTTACAAAACGAATATCATGTACA 1313


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Qy 1079 TGTGATTGACTATGCTGCCAATAATATCGGTGGCTGCAATGGCTGCTTCAACAG 1138
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Db 1436 ACTTGATAGACGGTGATTCGCTTCAAAATGTTGGTGGCTGGGGTTTTTGTCTAGTACAG 1495

Qy 1139 GAACGGACGCTGTCCCTTATTTTCGGATTTTAAATCCAATTATCCAGTCAAAAAATTTG 1198
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Db 1496 GAATTGATGCCCAACCATATTTTAGAGTTTTTTAATATGATATACAAGCAAAAAAATATG 1555

Qy 1199 ATAATGACGGCCAGTTTCATCAAAAAAATATGTCAGAACTTA 1240
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Db 1556 ACCACAATGATATTGTCAAACAATGGGTTCGCGAATTGA 1597

RESULT 15
US-09-489-039A-6144
; Sequence 6144, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6144
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6144

Query Match      8.2%; Score 117.4; DB 3; Length 1248;
Best Local Similarity 63.8%; Pred. No. 1.7e-22;
Matches 178; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 919 TGGCAAAAAGGGAGACGGGTACCTTATATGATCGCGCAATGCGACAACCTGAATCAA 978
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Db 967 TGGCAGCGCGGGAGACCGGTTTTCCGATTGTTGATCGGCCCATGCGCCAGCTTAACGCC 1026

Qy 979 ACTGTTGGATGCAACAATCGCTTAAGAATGATTACTGCCTCTTTTGTAGTTAAAAATTTA 1038
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1027 ACCGGCTGGATGCATACCGGTTACGCATGATTGTCGCCAGCTTCCTGACCAAGATTG 1086

Qy 1039 CACATCGAATTGGCGTTGGGGTGAAAAATACCTTCAAAAAAATGTTGATTGACTATGATGCT 1098
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1087 CGCCTCGACTGGCGGGCGGCGAGCGCTATTTCATGAGCCAGCTGATTGATGGCGACCTG 1146

Qy 1099 GCCAATAATATCGGTGGCTGGCAATGGCTTCAACAGAACGGACGCTGTCCCTTAT 1158
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Job time : 299 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2005, 17:38:08 : Search time 1284 Seconds
(without alignments)
9235.427 Million cell updates/sec

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Perfect score: 1434
Sequence: 1 atgaagagagataatggtt.....acaatccaagtttcaataa 1434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1434	100.0	1434	US-10-758-979-2	Sequence 2, Appli
2	1434	100.0	2267	US-10-758-979-1	Sequence 1, Appli
3	1432.8	99.9	5277	US-09-070-927A-262	Sequence 262, App
4	526.4	36.7	2460	US-10-398-221-3604	Sequence 3604, Ap
5	518.4	36.2	1163020	US-10-398-221-10	Sequence 10, Appl
6	518.4	36.2	3011208	US-10-398-221-2058	Sequence 2058, Ap
7	416.8	29.1	1451	US-10-398-221-1690	Sequence 1690, Ap
8	206.2	14.4	1393	US-08-781-986A-594	Sequence 594, App
9	206.2	14.4	1393	US-10-329-624-594	Sequence 594, App
10	199	13.9	1380	US-10-724-972A-3359	Sequence 3359, Ap
11	184.8	12.9	640881	US-09-790-988-1	Sequence 1, Appli
12	137.2	9.6	1698	US-10-793-639-226	Sequence 226, App
13	114.8	8.0	1404	US-09-738-626-701	Sequence 701, App
14	114.8	8.0	3309400	US-09-738-626-1	Sequence 1, Appli
15	104.2	7.3	1839	US-09-938-842A-479	Sequence 479, App
16	104.2	7.3	1839	US-09-938-842A-479	Sequence 479, App
17	100.4	7.0	3184	US-10-424-599-113803	Sequence 113803
18	99.2	6.9	1883	US-10-425-114-5586	Sequence 5586, Ap
19	99.2	6.9	2264	US-10-425-114-19130	Sequence 19130, A
20	99.2	6.9	2533	US-10-425-114-35600	Sequence 35600, A
21	99.2	6.9	2533	US-10-425-115-104197	Sequence 104197, A
22	99.2	6.9	2649	US-10-425-114-24312	Sequence 24312, A
23	99.2	6.9	2721	US-10-425-115-104199	Sequence 104199

Sequence 6341, Ap
Sequence 365, App
Sequence 182, App
Sequence 23734, A
Sequence 22489, A
Sequence 30074, A
Sequence 1201, Ap
Sequence 1, Appli
Sequence 1306, Ap
Sequence 124948,
Sequence 28413, A
Sequence 52170, A
Sequence 14400, A
Sequence 6319, Ap
Sequence 23273, A
Sequence 2479, Ap
Sequence 132131,
Sequence 52169, A
Sequence 425, App
Sequence 25806, A
Sequence 5999, A
Sequence 17600, A

ALIGNMENTS

RESULT 1
US-10-758-979-2
; Sequence 2, Application US/10758979
; Publication No. US20040214208A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Fredrick M.
; APPLICANT: Garsin, Danielle
; APPLICANT: Mylonakis, Eleftherios
; APPLICANT: Calderwood, Stephen B.
; APPLICANT: Sifri, Costi
; TITLE OF INVENTION: Enterococcal Virulence Factors
; FILE REFERENCE: 00786/408002
; CURRENT APPLICATION NUMBER: US/10758,979
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/22979
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,212
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1434
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-758-979-2

Query Match 100.0%; Score 1434; DB 8; Length 1434;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAAGAGTAATATGCTTTAGAGCTGATTTACGATTACAGGATAATAAGCATTAGCA 60
DB 1 ATGAAAGAGTAATATGCTTTAGAGCTGATTTACGATTACAGGATAATAAGCATTAGCA 60
QY 61 CACGGTTTACAAAATTTCTGCAGCTGATGAATGATTTTATTATTCCAAATGAATCCTCAA 120
DB 61 CACGGTTTACAAAATTTCTGCAGCTGATGAATGATTTTATTATTCCAAATGAATCCTCAA 120
QY 121 CAATTTATTCAGAAAGTGCCTTAATCATTAACGCTTTTTTTTTCGAGCTTAGCTCGTTCAA 180
DB 121 CAATTTATTCAGAAAGTGCCTTAATCATTAACGCTTTTTTTTTCGAGCTTAGCTCGTTCAA 180
QY 181 GAACGAATCGATCAGAGGACATTTACAATCATGTCGGCGAACCATTTAGATTATTTT 240
DB 181 GAACGAATCGATCAGAGGACATTTACAATCATGTCGGCGAACCATTTAGATTATTTT 240

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Qy 241 TCAGCTTTGAAACGCAAAATTACCGATTGGCAGGCCAATTATTTTAAATGAAGACTTGT 300
Db 241 TCAGCTTTGAAACGCAAAATTACCGATTGGCAGGCCAATTATTTTAAATGAAGACTTGT 300
Qy 301 GGCCTTTGGGCAAGCGGGAACAGCAAGCTATGCGCTTTTGAAGAAAAATAATATTAG 360
Db 301 GGCCTTTGGGCAAGCGGGAACAGCAAGCTATGCGCTTTTGAAGAAAAATAATATTAG 360
Qy 361 TCTTCTCTTTTCAAGTGCCTATTGTCATGGCTCTGAGAAATTAAGAAAGCATGGC 420
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Qy 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAAATGGAAGAGCGCCCTAAAGAAACA 480
Db 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAAATGGAAGAGCGCCCTAAAGAAACA 480
Qy 481 CCGATTCTGTTTCTATACAGCTGAAAAATTTTATAGTGGTGTCTTTTTTCCAGAAAGAG 540
Db 481 CCGATTCTGTTTCTATACAGCTGAAAAATTTTATAGTGGTGTCTTTTTTCCAGAAAGAG 540
Qy 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACACTATAGTGTGCGGAA 600
Db 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACACTATAGTGTGCGGAA 600
Qy 601 GAAACAGCGAAGCGCTTAAATCTTTTATGATCAAAAATTTCAATCTATGAAAAAT 660
Db 601 GAAACAGCGAAGCGCTTAAATCTTTTATGATCAAAAATTTCAATCTATGAAAAAT 660
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Db 661 AAGCGTGATTTTCTTATCAGGATCAAAACGAGTCACTGTCTACTTTTTTAAAGAACGGGA 720
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Db 721 GAACTTTTCGATTCGACCAATTTGCAAGAGCTTGCATCTGTGCTTCTAGCTTAAGTAAA 780
Qy 781 GAAACCTTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAGTGCCTTT 840
Db 781 GAAACCTTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAGTGCCTTT 840
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Db 841 CCAACAAACAAAGAGGAGCTATTCAAGAAAAATTTTGGTTATATTCAATGGACAAATGAC 900
Qy 901 CCAGAAATGTTTGTCAAGTGCACAAAGGAGAGCGGGTACCCCTATAAATGATGCGCGCA 960
Db 901 CCAGAAATGTTTGTCAAGTGCACAAAGGAGAGCGGGTACCCCTATAAATGATGCGCGCA 960
Qy 961 ATGCGACAACTGAATCAAACTGGTGGATGCACAAATCGCTTAAAGAAATGATTTACTGCGCTCT 1020
Db 961 ATGCGACAACTGAATCAAACTGGTGGATGCACAAATCGCTTAAAGAAATGATTTACTGCGCTCT 1020
Qy 1021 TTTTATAGTTAAAAATTTACACATCGATTGGCGTTGGGGTGAAAAATACTTTTCAAAAAATG 1080
Db 1021 TTTTATAGTTAAAAATTTACACATCGATTGGCGTTGGGGTGAAAAATACTTTTCAAAAAATG 1080
Qy 1081 TTGATTGATATGATGTCGCAATAATATCGTGGCTGGGCAATGGGCTGCTTCAACAGGA 1140
Db 1081 TTGATTGATATGATGTCGCAATAATATCGTGGCTGGGCAATGGGCTGCTTCAACAGGA 1140
Qy 1141 ACGCAAGCTGTCCCTTATTTTTCGGATTTTAAATCCCAATTTATCCAGTCAAAAAATTTGAT 1200
Db 1141 ACGCAAGCTGTCCCTTATTTTTCGGATTTTAAATCCCAATTTATCCAGTCAAAAAATTTGAT 1200
Qy 1201 AATGACGCCAGTTTCATCAAAAAATATGTTTCCAGAACTTAAGCAAGTGCCACAAAAAGTAT 1260
Db 1201 AATGACGCCAGTTTCATCAAAAAATATGTTTCCAGAACTTAAGCAAGTGCCACAAAAAGTAT 1260
Qy 1261 ATTCAATCAACCAATCTAATGAACGAAGCCCTTACAAACGCAATATCATGTACATTTAGGA 1320
Db 1261 ATTCAATCAACCAATCTAATGAACGAAGCCCTTACAAACGCAATATCATGTACATTTAGGA 1320
Qy 1321 GAAAAATTATCAAAAACCCATTGTGATTTATGTCATCAAGTAAAAACAAACATTGTTTCTA 1380
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Db 1321 GAAAAATTATCAAAAACCCATTGTGATTTATGTCATCAAGTAAAAACAAACATTGTTTCTA 1380
Qy 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAAATCCAAAGGTTTCAATAA 1434
Db 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAAATCCAAAGGTTTCAATAA 1434

RESULT 2
US-10-758-979-1
; Sequence 1, Application US/10758979
; Publication No. US20040214208A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Fredrick M.
; APPLICANT: Garsin, Danielle
; APPLICANT: Mylonakis, Eletherios
; APPLICANT: Calderwood, Stephen B.
; APPLICANT: Sifri, Costi
; TITLE OF INVENTION: Enterococcal Virulence Factors
; FILE REFERENCE: 00786/408002
; CURRENT APPLICATION NUMBER: US/10/758,979
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/22979
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,212
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-758-979-1

Query Match 100.0%; Score 1434; DB 8; Length 2267;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAAGAGTAATATGTTTAGCGTTTAGCGATTACGATTACAGGATTAAGAGCATTAGCA 60
Db 568 ATGAAAAGAGTAATATGTTTAGCGTTTAGCGATTACGATTACAGGATTAAGAGCATTAGCA 627
Qy 61 CAGCGGTTACAAAATTTCTGCAGCTGATGAATGATTTTATTTATTCAAAATGAATCTCTCAA 120
Db 628 CAGCGGTTACAAAATTTCTGCAGCTGATGAATGATTTTATTTCCAAATGAATCTCTCAA 687
Qy 121 CAATTTATTTCAAGAAAGTGCTAATATAACGCTTTTTTTTGCAGCTTAGCGCTCGTTCAAA 180
Db 688 CAATTTATTTCAAGAAAGTGCTAATATAACGCTTTTTTTTGCAGCTTAGCGCTCGTTCAAA 747
Qy 181 GAACGAATCGATCAAGAGGCACATTTTACAAATCATGGTGGCGGAAACATTAGATTTATTT 240
Db 748 GAACGAATCGATCAAGAGGCACATTTTACAAATCATGGTGGCGGAAACATTAGATTTATTT 807
Qy 241 TCAGCTTTGAAACGCAAAATTTACCCGATTTCGAGCGCAATTTATTTTAAATGAAGACTTGT 300
Db 808 TCAGCTTTGAAACGCAAAATTTACCCGATTTCGAGCGCAATTTATTTTAAATGAAGACTTGT 867
Qy 301 GGCTTTGGGCAAGCGGACCGGACCGAGCAAGCTATGCGCTTTTTTGAAGAAAAATAATATTAG 360
Db 868 GGCTTTGGGCAAGCGGACCGGACCGAGCAAGCTATGCGCTTTTTTGAAGAAAAATAATATTAG 927
Qy 361 TCTTCTCTTTTCAAGATGCTATTGTCATGGCTCTGAGAAATTAAGAAAGCATGGC 420
Db 928 TCTTCTCTTTTCAAGATGCTATTGTCATGGCTCTGAGAAATTAAGAAAGCATGGC 987
Qy 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAAATGGAAGAGCGCCCTAAAGAAACA 480
Db 988 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAAATGGAAGAGCGCCCTAAAGAAACA 1047
Qy 481 CCGATTCTGTTTCTTATACAGCTGAAAAATTTTATAGTGGTGTCTTTTTTCCAGAAAGAG 540
Db 1048 CCGATTCTGTTTCTTATACAGCTGAAAAATTTTATAGTGGTGTCTTTTTTCCAGAAAGAG 1107
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QY 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAACACACTATAGTGTGGCGAA 600
DB 1108 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAACACACTATAGTGTGGCGAA 1167
QY 601 GAAACAGCCAGAGGCGCTTAAATCTTTTATGATCAAAAACCTTCAATCTATGAAAT 660
DB 1168 GAAACAGCCAGAGGCGCTTAAATCTTTTATGATCAAAAACCTTCAATCTATGAAAT 1227
QY 661 AAGCGTGATTTTCTTATCAGATCAAAACGAGTCACTGTCTACTTTTAAAGACGGGA 720
DB 1228 AAGCGTGATTTTCTTATCAGATCAAAACGAGTCACTGTCTACTTTTAAAGACGGGA 1287
QY 721 GAACTTTCGATTCGACCACTTGGCAAGCTTGGCATCTGTGCTCTAGCTTAAGTAA 780
DB 1288 GAACTTTCGATTCGACCACTTGGCAAGCTTGGCATCTGTGCTCTAGCTTAAGTAA 1347
QY 781 GAAACCTTCAAAAAGAAATTAGCTTGGCGCGACTTTTACAATATGATCTATAGTGGCTTT 840
DB 1348 GAAACCTTCAAAAAGAAATTAGCTTGGCGCGACTTTTACAATATGATCTATAGTGGCTTT 1407
QY 841 CCAACAAAAAGAGGAAGCTATTCAAGAAAAATTTCTGTATTTCAATGGACAAATGAC 900
DB 1408 CCAACAAAAAGAGGAAGCTATTCAAGAAAAATTTCTGTATTTCAATGGACAAATGAC 1467
QY 901 CCAGAAATGTTGTCAAGTGGCAAAAAGGGGAGACGGGTACCTTAAATTTGATGCGCGA 960
DB 1468 CCAGAAATGTTGTCAAGTGGCAAAAAGGGGAGACGGGTACCTTAAATTTGATGCGCGA 1527
QY 961 ATGCGACAACTCAATCAAACTGGTGGATGCAATCGCTTAAAGATGATTAAGTGGCTCT 1020
DB 1528 ATGCGACAACTCAATCAAACTGGTGGATGCAATCGCTTAAAGATGATTAAGTGGCTCT 1587
QY 1021 TTTTGTAGTTAAAAATTTACATCGATTTGGCGTGGGGTGAAAAATCTTTCAAAAAATG 1080
DB 1588 TTTTGTAGTTAAAAATTTACATCGATTTGGCGTGGGGTGAAAAATCTTTCAAAAAATG 1647
QY 1081 TTGATGACTATGATGCTGCCAATATATCGTGGTGGCAATGGCTGCTTCAACAGA 1140
DB 1648 TTGATGACTATGATGCTGCCAATATATCGTGGTGGCAATGGCTGCTTCAACAGA 1707
QY 1141 ACGGAGCTGCTCCCTTATTTTCGGATTTTAAATCCAAATTTATCCAGTCAAAAAATTTGAT 1200
DB 1708 ACGGAGCTGCTCCCTTATTTTCGGATTTTAAATCCAAATTTATCCAGTCAAAAAATTTGAT 1767
QY 1201 AATGACGGCCAGTTCAATCAAAAAATATGTTCCAGAACTTTAAGCAAGTGCCACAAAAGTAT 1260
DB 1768 AATGACGGCCAGTTCAATCAAAAAATATGTTCCAGAACTTTAAGCAAGTGCCACAAAAGTAT 1827
QY 1261 ATTCAATCAACCAATCTAATGAACGAGCCTTACAAACGCAATATCATGTATAGGA 1320
DB 1828 ATTCAATCAACCAATCTAATGAACGAGCCTTACAAACGCAATATCATGTATAGGA 1887
QY 1321 GAAATTTCCAAACCCATTTGCGATTTATGATGATCAAGTAAACCAACATTTGTTCTTA 1380
DB 1888 GAAATTTCCAAACCCATTTGCGATTTATGATGATCAAGTAAACCAACATTTGTTCTTA 1947
QY 1381 TATGAAGCGCAGCAAGAAATTTATCAAGAAATGAACAAATCCAAAGGTTTCAATAA 1434
DB 1948 TATGAAGCGCAGCAAGAAATTTATCAAGAAATGAACAAATCCAAAGGTTTCAATAA 2001

RESULT 3
US-09-070-927A-262
; Sequence 262, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; Patrick J. Dillon
; Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 262:
SEQUENCE CHARACTERISTICS:
LENGTH: 5277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 262:
US-09-070-927A-262
Query Match 99.9%; Score 1432.8; DB 3; Length 5277;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1431; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAAAAGAGTAATATGTTTAGACGTGATTACGATTACAGGATAATAAAGCATTAGCA 60
DB 1046 ATGAAAAAGAGTAATATGTTTAGACGTGATTACGATTACAGGATAATAAAGCATTAGCA 1105
QY 61 CACCGTTACAAAATCTGACAGCTGATGAATGATTTTATTTCCAAATGAATCCTCAA 120
DB 1106 CACCGTTACAAAATCTGACAGCTGATGAATGATTTTATTTTCCAAATGAATCCTCAA 1165
QY 121 CAATTTATTCAGAAAGTGTCTAATCATACGCTTTTTTTTGCAGCTTAGCCTCGTTCAA 180
DB 1166 CAATTTATTCAGAAAGTGTCTAATCATACGCTTTTTTTTGCAGCTTAGCCTCGTTCAA 1225
QY 181 GAACGAATCGATCAAGAGGCACTTTACAAATCATGTGCGGCAACCAATTAGATTTATTT 240
DB 1226 GAACGAATCGATCAAGAGGCACTTTACAAATCATGTGCGGCAACCAATTAGATTTATTT 1285
QY 241 TCAGTTTGAACACGCAATTAACCGATTTGGCAGGCAATTTATTTTAAATGAAGATACCTGT 300
DB 1286 TCAGTTTGAACACGCAATTAACCGATTTGGCAGGCAATTTATTTTAAATGAAGATACCTGT 1345
QY 301 GGCTTTGGGCAAGCGGACGACGATGCGCTTTTTTTTGAAGAAAAATAATATTCAG 360
DB 1346 GGCTTTGGGCAAGCGGACGACGATGCGCTTTTTTTTGAAGAAAAATAATATTCAG 1405
QY 361 TCTTTCTCTTTTCAAGATGCGCTATTGTCATGGCTCTGAAGAAATTTAAGAAAGCAATGGC 420
DB 1406 TCTTTCTCTTTTCAAGATGCGCTATTGTCATGGCTCTGAAGAAATTTAAGAAAGCAATGGC 1465
QY 421 AGCAAGTACCAAGTGTGTTTACGCCCTTATTAATAATCGAAAGAGCGCCCTTAAAGAAACA 480
DB 1466 AGCAAGTACCAAGTGTGTTTACGCCCTTATTAATAATCGAAAGAGCGCCCTTAAAGAAACA 1525

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QY 481 CCGATTCTGTTTCTATACAGCTGAAGAAATTTTATAGTGGTGTCTTTTCCAGAGAG 540
Db 1526 CCGATTCTGTTTCTATACAGCTGAAGAAATTTTATAGTGGTGTCTTTTCCAGAGAG 1585
QY 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAAACACACTAGTGTGCGGAA 600
Db 1586 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAAACACACTAGTGTGCGGAA 1645
QY 601 GAAACAGCCAGAGCGCTTAAATACTTTTATGATCAAAAACCTTCAATCCTATGAAAT 660
Db 1646 GAAACAGCCAGAGCGCTTAAATACTTTTATGATCAAAAACCTTCAATCCTATGAAAT 1705
QY 661 AAGCGTGATTTTCTTATCAGATCAGACGAGTCTGCTACTTTTAAAGAACGGA 720
Db 1706 AAGCGTGATTTTCTTATCAGATCAGACGAGTCTGCTACTTTTAAAGAACGGA 1765
QY 721 GAACTTTTCGATTCGACCATTTGGCAAGAGCTTGCACTGTGCTCTTAGCTTAAGTAA 780
Db 1766 GAACTTTTCGATTCGACCATTTGGCAAGAGCTTGCACTGTGCTCTTAGCTTAAGTAA 1825
QY 781 GAAACCTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAATATGATCTATAGTGGTTT 840
Db 1826 GAAACCTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAATATGATCTATAGTGGTTT 1885
QY 841 CCACACAAAGAGGAGCTATTCAAGAAAATTTTGGTTATATCAATGACAAATGAC 900
Db 1886 CCACACAAAGAGGAGCTATTCAAGAAAATTTTGGTTATATCAATGACAAATGAC 1945
QY 901 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGTACCCCTATAATTTGATGCGCA 960
Db 1946 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGTACCCCTATAATTTGATGCGCA 2005
QY 961 ATGGACAACTGAATCAAACTGGTTGGATGACAAATCGCTTAAAGATGATCTGCTCT 1020
Db 2006 ATGGACAACTGAATCAAACTGGTTGGATGACAAATCGCTTAAAGATGATCTGCTCT 2065
QY 1021 TTTTGTAGTAAATTTTACACATCGATTTGGGTTGGGTGAAATACCTTCAAAAATG 1080
Db 2066 TTTTGTAGTAAATTTTACACATCGATTTGGGTTGGGTGAAATACCTTCAAAAATG 2125
QY 1081 TTGATTGATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA 1140
Db 2126 TTGATTGATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA 2185
QY 1141 ACGGACGTGCTCTTATTTTCGATTTTAAATCCAAATATCCAGTCAAAAATTTTAT 1200
Db 2186 ACGGACGTGCTCTTATTTTCGATTTTAAATCCAAATATCCAGTCAAAAATTTTAT 2245
QY 1201 AATGACGCCAGTTTCATCAAAAATATGTTCCAGAACTTAAGCAAGTGGCCACAAAGTAT 1260
Db 2246 AATGACGCCAGTTTCATCAAAAATATGTTCCAGAACTTAAGCAAGTGGCCACAAAGTAT 2305
QY 1261 ATTCAATCAACCAATCTAATGAACGAGCCCTTACAAAGCCAAATCATGTACATTTAGGA 1320
Db 2306 ATTCAATCAACCAATCTAATGAACGAGCCCTTACAAAGCCAAATCATGTACATTTAGGA 2365
QY 1321 GAAATATCAAAACCCATTTGATTTATGATGATCAAGTCAAAAGGCAAAATGTTTCTA 1380
Db 2366 GAAATATCAAAACCCATTTGATTTATGATGATCAAGTCAAAAGGCAAAATGTTTCTA 2425
QY 1381 TATGACGCGAAGAAATTCATCAAGAAATGAACAAATCCAGGTTTCAATA 1434
Db 2426 TAKGAAGCGACGAAGAAATTCATCAAGAAATGAACAAATCCAGGTTTCAATA 2479
```

RESULT 4

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US-10-398-221-3604
; Sequence 3604, Application US/10398221
; Publication No. US200400185141
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
```

```
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3604
; LENGTH: 2460
; TYPE: DNA
; ORGANISM: Listeria monocytogenes 4b
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3604
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Query Match 36.7%; Score 526.4; DB 7; Length 2460;
Best Local Similarity 61.6%; Pred. No. 4.9e-117;
Matches 883; Conservative 0; Mismatches 536; Indels 15; Gaps 2;

QY 1 ATGAAAAGAGCTAATATGTTTACAGCTGATTACGATTACAGATATAAAGCATTAGCA 60
Db 241 ATGACTTCGTAATGTTTTCGGAGAGATCTTCGAGTAAACGATATAAAGCTCTCTAT 300
QY 61 CACGCGTTACAAAATTTCTGAGCTGATGAATGATTTTATTTTCCAAATGAATCTCTCA 120
Db 301 CATGC-----TTGTAAGAGGACGATTTGCTTTTGTATTTCAGTAAATCCAGCA 351
QY 121 CAATTTATTCAGAAAGTGTCTAATCATACAGCTTTTTTTTTCGAAGCTTAGCTGTTCAA 180
Db 352 CAGTTTCATCACAGAAAGTCTTAGCCACCAAGCTTTTTTTTTCGAAGTGTGGCTCATTTA 411
QY 181 GAACGATCGATCAAGAGGCACATTTACAAATCATGTGCGCGAACCATTAGATTTATTT 240
Db 412 CAAGAAATCGATAAAACTGGCAATTTTACAAATCATGTTTGGTGAACGATAGATGCTTC 471
QY 241 TCACGTTTGAACCGCAAAATTTACCCGATTGGCAGGCCATTTATTTTAAATGAAGATCT 300
Db 472 CAACAACCTTAAAGATTCGCTACCAAGCTGGGATAAAGTTTATTTTCAACCGTGAAGAA 531
QY 301 GGCCTTTGGGCAAGCGGACAGCAAGCTATGCGCTTTTTTTTGAAGAAATATATATTCAG 360
Db 532 GGATACGGAGCAAGCGGGATGAGCGCGCAAGCGTTCTTTTGACGAACAAAATTCGAG 591
QY 361 TCTTTCTCTTTTCAAGATGCTATTATTTGATGGCTCTGAAGAAATTAAGAAAGACGATGG 420
Db 592 GTTCAAGCCTTCCAGATAGCTATCTTCAATCAGCGGAAGAGTAAGAAATCTCCNACA 651
QY 421 AGCAAGTACCAAGTGTTTAGCCCTATTACAATTAATGGAAGAGGCGCTTAAAGAAACA 480
Db 652 GAATACTATAAAATTTTATCCCTTATATAAAATATGGCGGAAGAAATAAAGAAACG 711
QY 481 CCGATTCCTGTTTCTTATACAGCTGAAAATTTTTTTAGTGGCTGTCTTTTTCCAGAGAG 540
Db 712 CCGTTCAAAAGTGACTTTTAAAGCATGAGAAATATCCGAAAAGAAAGCTTTGTTTCTGA 771
QY 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACACTATATAGTGTGG 600
Db 772 GAAGAACAATTTCCGGAATATGACT-----AGCGATTTACCGATATTAGATATTGGTGA 825
QY 601 GAAACAGCCAGAGAGCGCTTAAATACTTTTATTTGATCAAAAACCTTCAATCCTATGAAAT 660
Db 826 CGAGCAGCGAAACACGAGACTTGGGAATTTTATTAACACGATGTGCTGACTATGACAAA 885
QY 661 AAGCGTGATTTTCTTATCAGGATCAAAACGATCATCTGCTACTTTTTTAAAGAACGGA 720
Db 886 CGAGAGAGATTTTCCGGAACCTGGATAAAAACAAAGCCATTTATACAGTATTATTCACGA 945
QY 721 GAACTTTTCGATTCGCCACCATTTTGGCAAGAGCTTGGCATCTGTGCTCTTAGCTTTAAGTAA 780
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946	DB	GAATCTCGATT	CGGACGATTTGGCAGACACITTTCAAGAAACAGAAAGCAACAGAAAGACGA	1005
781	QY	GAACCTTC	CAAAAAGAAATTAGCTTCGCGCGACTTTTCAATATATGATCTATAGTGGTGT	840
1006	DB	GCTACATTTG	AAAAGAACTGTGTAGCGCGACTTTTATATATGATTTACGTTCTTTT	1065
841	QY	CCAAACAAAAG	AGGAAGCTATTTCAGAAAAAATTCGTTATATCAATGGAACAAATGAC	900
1066	DB	CCTAACCAAAA	AACGAGCGGATCCAGAAAAATATCGTTTATTCGAATGGGAAAAATAAC	1125
901	QY	CCAGAAATGTT	TCAGTGGCAAAAAGGGAGACGGGTACCCCTATAATTCGATGCCGA	960
1126	DB	CGCGAAATAT	TTCAAAGCGTGGCAAGAAAGGAAGACTGGTTTCCCGCTCGTTGATCGGGC	1185
961	QY	ATCGGACAACT	GAATCAAACTGGTGGATGCACAAATCGCTTAAGAAATGATTAAGTCCCTCT	1020
1186	DB	ATCGCGCAGTT	GAAGAACTGGTTGGATGCATAATCGACTAAGATGATTAACGGGTCC	1245
1021	QY	TTTTTTAGTT	AAAAATTTACACATCGAATGGCGTTGGGGTGAAAAATACTTTTCAAAAAATG	1080
1246	DB	TTTTTAAACA	AAAGATTTGCTGATTTGATGGCGTTTTTGGCAAAAAGTATTTTCAACAAATG	1305
1081	QY	TTGATTGACT	ATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA	1140
1306	DB	CTGATTGATT	GATATCCTCGCAGTAATTTGGTGGCTGGCAATGGGCGGCTTCGACTGGA	1365
1141	QY	ACGGACGCTG	TCTCTATTTTTCGGATTTTTTAATCCAAATTAATCCAGTCAAAAAAATTTGAT	1200
1366	DB	ACGGATCGGT	GCGCATACTTTAGGATTTTCAACCCACAGCACAAATCACAAAAATTTGAT	1425
1201	QY	AATGACGGCC	AGTTTCATCAAAAAATATGTTTCCAGAACTTAAGCAAGTGCCACAAAAGTAT	1260
1426	DB	TCGACTGGGA	AAATTTATTCGAAAAATATGTAAAAAGAGTTAGCGAATCTACCTGATAAATAT	1485
1261	QY	ATTTCATCAA	CCAAATCTAATGAACGAGCCCTTACAAAGCAATATCATGTACATTTAGGA	1320
1486	DB	ATTTCATCAA	CCAGAAAAAATGTCCAGAACTGAGCAGAAAGAGCATGGCTTGCTGTAGGA	1545
1321	QY	GMAAATTTAT	CCMAAACCCATTTGCTGATTTATGTCATCAAGTAAAAAACAACATTTGTTCTA	1380
1546	DB	AAAGACTAT	CCATTTTCCGATAGTTGACCATAAAGAACGACGGAAATTAGCCATTGCAAGC	1605
1381	QY	TATGAAGCG	AGCAAGAAATTCATCAAGAAATGAACAAATCCAGGTTTCAATAA	1434
1606	DB	TACGAGTTT	AGCAAGAGCATTTAGGGGAAATATAGATAATAGACTCAATCA	1659

RESULT 5

Qy	661	AAGCGTGATTTTCCCTTATCAGGATCAAAACGAGTCACTGTCTACTCTTTTAAAGAACGGGA	720
Db	538460	GCAAGAGACGCTCCAGCGCTTGATAAACGAGTCATTATCAGCGTATTTATACGAACGGGA	538519
Qy	721	GAACTTTGATTTGCGACCATTTTGGCAAGAGCTTGTCCTTCTAGCTTAAGTAAA	780
Db	538520	GAGATTTGATTTGCTACGCTTTGGCAGGCACTTCAAAAAGAGAAAGCTACAGAAGGACGA	538579
Qy	781	GAAACCTTCAAAAAAGAAATAGCTTTGGCGGCACTTTTACAAATATCATCTATAGTCGCTTT	840
Db	538580	GCAACATTCGAAAAAGAACTGTGTTGGCGCGATTTTTATATATGATTTATGTTCTTTT	538639
Qy	841	CCACAACAAAAAGAGGAAGCTATTCAAGAAAAATTTTCGTTATATTTCAATATGGAACAATGAC	900
Db	538640	CCAAAGCAAAAAAATGAGCCTATTCAAGAAAAATTTATCGTTTTATTGAAATGGGAAAAATAAT	538699
Qy	901	CCAGAAATGTTTGTCAAGTGGCAAAAAAGGGGACGGGTACCTATATAATTGATGCCCGCA	960
Db	538700	CGCGAATTTTTTCAAGAAGTGGCAAGACGGGCAAACTGGTTTTCCGCTTGTGATGCTCGG	538759
Qy	961	ATGCGACAACACTGAATCAAACTCGTTTGGATGCAACAATCGCTTAAAGAAATGATTACTGCTCT	1020
Db	538760	ATGCGCCAATTTAAAGAGACGGGCTGGATGCATATACGCTAAAGAATGATCAGGCTTCC	538819

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QY 1021 TTTTGTAGTTAAATTTACACATCGATTGGCGTTGGGTTGGAATACTTTTCABAATG 1080
Db 538820 TTTTAAACGAAGGATTTTACTAATTGATTGGCGTTTGGCGAAATAATTTTCAACAATG 538879
QY 1081 TTGATTGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA 1140
Db 538880 CTAATTGATTACGACCCAGCGAGTAATATTGGCGTTGGCAGTGGCGGCTTCGACTGGA 538939
QY 1141 ACGGACGCTGCCCTTATTTTCGGATTTTAAATCCAATTTATCCAGTCAAAAAATTTGAT 1200
Db 538940 ACAGATGAGTACCGTATTTTAGAATTTTAAATCCAACCAACCAATCGGAAAAATTTGAT 538999
QY 1201 AATGACGCCAGTTTCATCAAAAATAATGTTCCAGACTTAAGCAAGTGGCCACAAAAGTAT 1260
Db 539000 CCAGATGTATCATTTATTTCGGAATATATGTAAGGAATTTACGGGACTTGC CGGATAAATTC 539059
QY 1261 ATTCATCAACCAATCTAATGAACGAGCCTTACAAACGCAATATCATGTACATTTAGGA 1320
Db 539060 ATTCATCAACCAAAAATGCTGAAACACAGACAAAAGAGCATGGTTGATTTTAGGA 539119
QY 1321 GAAATTTATCCAAACCCATTTGTCGATTTATGATTCATCAAGTAAAGTAAACAAATGTTCTA 1380
Db 539120 AAAGATTATCGCTTCGGATAATCGACCATAAAGAGCGACGAAAAATTAGCGATTGCGGA 539179
QY 1381 TATGACGCGCAAGAATTCATCAAGAAATGAACATCCAAGTTTCAATA 1434
Db 539180 TATGAGTTTAGCAAGGAGCATTTAGGGAAATATATAGATAATGAATCAATCA 539233

RESULT 6
US-10-398-221-2058
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398, 221
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2058
; LENGTH: 3011208
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2058

Query Match 36.2%; Score 518.4; DB 7; Length 3011208;
Best Local Similarity 61.2%; Pred. No. 1.4e-113;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

QY 1 ATGAAAAGAGTAATATGTTTAGACGTGATTTACGATTACGATTACAGGATAATAAGCAATTAGCA 60
Db 628080 ATGACTTCAGTAATGTGGTTTCGTAGAGATCTTCGAGTAATGATAATAAAGCTCTTTAT 628139
QY 61 CACGGTTACAAAATCTGACAGCTGATGATTTGATTTTATTTATTCGAATGATCCCTCAA 120
Db 628140 CATGCCGTGTAAGA-----AGAAAGATTAAATTTGTTATTTCGAAGTAATCCAGNA 628190
QY 121 CAATTTATTCAAGAAAGTGCTAAATCAAAACGCTTTTTTGTGCAAGCTTAGCCTCGTTCAAA 180
Db 628191 CAATTTATCAAGGAGGCCCTAGTCACCAAGCATTTTTCGGAGTGTAGCTATTTTCAA 628250
QY 181 GAACGAATCGATCAAGAGGCACTTTTACAAATCATGTCGCGCAACCATTAGATTTATTT 240
Db 628251 CAAGAACTAAATAAAAAACACCCATTTGCAATCATGTTTGGCGAGCCAAATCGAGCTCTTA 628310
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QY 241 TCACGTTTGAACGCAAAATTACCGGATTTGGCAGGCCAATTTATTTTAAATGAAGACTTGT 300
Db 628311 AAACAATTAAGAAAGAAAATAACCAACTTGGGATAAAGTTTTTCTTCAACCGGATGAACA 628370
QY 301 GGCTTTGGGCAAGCGGGAACAGCAAGCTATGCGCTTTTGAAGAAAAATAATATTTCAG 360
Db 628371 GGCTACGGAGCGAGTCGAGACGAGGCTGCCGAGCACTTCTTCTGATAGGAAATCACCA 628430
QY 361 TCTTCTCTTTTCAAGATGCTATTTGTCATGGCTCTGAGAGAAATTAAGAAAGACGATGGC 420
Db 628431 GTTTCAGAGCTATCACGATAGTTTACCTTCTATTCAGCTGAAGAGTGAAGAAAATCCGCCA 628490
QY 421 AGCAAGTACCAGCTGTTTACGCCCTTATCAATAAATGGAAGAGCGCGCTAAAGAAACA 480
Db 628491 GAATATCAAAAATCTTCACTCTCTTACAAAATAATGGCGCGAAGAAATAAAGAAATG 628550
QY 481 CCGATTCTCTGTTTCTATACAGCTGAAAAAATTTTATGTCGCTGTCTTTTCCAGAAAGAG 540
Db 628551 CCTTTAAAGTCACTTTAAAAACGAGAAAAAATTTAGGAAAGAAAGCTTATTTCCAAATAT 628610
QY 541 GAAGCAGCTTATCGTGAACAGATTGGAGGATTCCTTTTAAACACACTATAGTGTGCGGAA 600
Db 628611 GAGGAACAGTTTATAGAACTGATTT-----CAAGATTTTACAGCCTTTGATTCGGGTGAA 628664
QY 601 GAAACAGCGAAGAGCGCTTTAAATACTTTTATTTGATCAAAAACTTCAATCTTATGAAAA 660
Db 628665 AAAGCAGCGAATACGAGACTTGCAAAATTTTGAAGAAAGATTTAGCAGACTATGACAAA 628724
QY 661 AAGCGTATTTCTCTTATCAGGATCAAAAGAGTCATCTGTCTACTTTTAAAGAACGGGA 720
Db 628725 GCAAGAGAGCTCCAGCGCTTGATAAAAACGAGTCAATTTATCACGCTATTTACGAAACGG 628784
QY 721 GAATTTTCGATTCGACCATTTTGGCAAGAGCTTGCATCTGTGCTTCTAGCTTTAAGTAAA 780
Db 628785 GAGATTTTCGATTCGTTTGGCAGGCACTTTCAAAAAAGAAAGCTACAGAAAGACGA 628844
QY 781 GAAACCTTCAAAAAAGAAATTTAGCTTGGCGGACTTTTACAAATATGATCTATAGTGCCTT 840
Db 628845 GCAACATTCGAAAAGAACTGTGTTTGGCGGATTTTATATATGATTTATGTTCTTTT 628904
QY 841 CCAACAAAAAGAGGAAGCTATTTCAAGAAAAATTTTCGTTATATTCAATGACACAAATGAC 900
Db 628905 CCAAGCAAAAAAATGAGCCTATTTCAAGAAAAATTTATCGTTTTTATGAAATCGGAAAAAT 628964
QY 901 CAGAAAATGTTTGTCAAGTGGCAAAAGGGGACACGGGTACCTATATTTGATGCGGCA 960
Db 628965 CGCGAATTTTTCAGAAAGTGGCAAGACGGGCAAACTGGTTTTCCGCTTGTTCGATGTGCG 629024
QY 961 ATGCGACAACTGAATCAAACTGGTTGGATGCAAACTCGCTTAAAGAAATGATTACTGCTCT 1020
Db 629025 ATGCGCAATTAAGAGAGACGGCTGGATGCAATTCGGCTAAGATATGATCAAGGCTTCC 629084
QY 1021 TTTTATGTTAAAAATTTTACACATCGATTGGCGTTGGGTTGGAATAATACTTTCAAAAAATG 1080
Db 629085 TTTTAAACGAAGGATTTTACTAATTTGATTTGGCGTTTTTGGGAAAAATAATTTTCAACAAATG 629144
QY 1081 TTGATTGACTATGATGCTGCCAATAATAATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA 1140
Db 629145 CTAAATGATTTACGACCCAGCGAGTAATATTGGCGGTTGGCAGTGGGCGGCTTCGACTGGA 629204
QY 1141 ACGGACGCTGCTCTTATTTTTCGATTTTAAATCTCAATTTATCCAGTCAAAAAATTTGAT 1200
Db 629205 ACAGATGCGAGTACCGTATTTTAGAATTTTATCCAAACCAACCAATTCGGAATAATTTGAT 629264
QY 1201 AATGACGGCCAGTTCATCAAAAAATAATGTTTCCAGAACTTAAGCAAGTGGCCACAAAAGTAT 1260
Db 629265 CCAGATGGTACATTTATTCGGAATAATGTAAGGAATTTACGGGACTTGC CGGATAAATTC 629324
QY 1261 ATTTCATCAACCAATCTAATGAACGAGCCTTTACAAACGCAATATCATGTACATTTAGGA 1320
Db 629325 ATTTCATCAACCAAAAAAATGCTGTAACAGAGCAAAAAAGAGCATGGTTGATTTTAGGA 629384
QY 1321 GAAATTTATCCAAAAACCCATTTGTCGATTTATGCAATCAAGTAAAAAACAACATTTGTTCTA 1380
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Db 629385 AAAGATTATCGCTTCGATTAATCGACATTAAGAGCGGACGAAATTAGCGATTGCGGA 629444
Qy 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAAATCCAGGTTTCAATAA 1434
Db 629445 TATGAGTTTAGCAAGGAGCAATCTAGGGGAAATATATAGATAATGAATCAATCA 629498

RESULT 7

US-10-398-221-1690
; Sequence 1690, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: PC7/FR 01/03 061
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1690
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Listeria monocytogenes-4B
US-10-398-221-1690

Query Match 29.1%; Score 416.8; DB 7; Length 1451;
Best Local Similarity 59.0%; Pred. No. 1.6e-90;
Matches 759; Conservative 0; Mismatches 512; Indels 15; Gaps 2;

Qy 1 ATGAAAGAGTAATATGGTTTATAGCTGATTTACGATTACAGGATAATAAGCAATTAGCA 60
Db 39 ATGACTTCGGTANTGGTTTCGGAGAGATCTTCAGTAACGATAATTAAGCTCTCTAT 98
Qy 61 CACGGGTTACAAAATTTCTGACCTGATGAATGATTTTATATATCCAAATGAATCCTCAA 120
Db 99 CATGC-----TTGTAAGAGAGGACGATTTGCTTTTGTATTTCAAGTAAATCCAGCA 149
Qy 121 CAATTTATTAAGAAAGTCTAATCATACGCTTTTTCGAACTTTTTCGAACTTACCTCGTTCAA 180
Db 150 CAGTTTCATCAGGAAGTCTTAGCCACCAAGCTTTTTCGAACTTACCTCGTTCAA 209
Qy 181 GAACGATCGATCAGAGGACGATTTACAAATCATGCTCGGCGAACCATTTAGATTTATTT 240
Db 210 CAAGAAATCGATAAAACTCGGCATTTACAAATCATGTTTGGTGAACCGTAGAATGCTTC 269
Qy 241 TCACGTTTCAAAACGCAAAATTTACCGATTTGGCAGGCGCATTTATTTAATGAAGATCTGT 300
Db 270 CAACAACTTAAGATTCGCTACCAAGCTGGGATAAGTTTATTTCAACCGTATGAACAA 329
Qy 301 GCGTTTGGGCAAGAGCGGACGAGCAAGCTATGCGCTTTTTCGAAAGAAATTAATTCAG 360
Db 330 GGATACGAGCAAGAGCGGATGAGCGGCGCAAGCGTTTCTTTCGCAACAAAATTCGAG 389
Qy 361 TCTTTCTCTTTTCAAGATGCTATTTGCTGCTGTAAGAAATTAAGAAAGAACGATGCG 420
Db 390 GTTCAAGCGCTTCACGATAGTATCTTCATTCAGCGGAAGAGTAAGAAATTCCTCAAC 449
Qy 421 AGCAAGTACCAAGTGTTCAGGCGCTATTACAAATAAATGAAAGAGCGGCTTAAGAAACA 480
Db 450 GAATCTATAAATTTTACCCCTTATTAATAAATGCGCGAAGAAATAAAGAAAGCG 509
Qy 481 CCGATTCCTGTTTCCATATACGCTGAAATAATTTTTCGCTGCTTTTTCAGAGAG 540
Db 510 CCGTTCAAGTGCATTTAAAGCATGAGAAATATCCGGAAGAAAGAGCTTGTTCGAAATAT 569
Qy 541 GAAGCAGCTTATCGTGAACAGATTCGAGGATTTCTTTTAAACACACTATAGTTCGCGGAA 600

Db 570 GAAGAACAAATTTCCGGAATGACT-----AGCGATTACCGATATATAGATATTGGTGAA 623
Qy 601 GAAACAGCCAGAGAGCGCTTAAATACTTTTATGATCAAAAATCTCAATCTCTATGAAAT 660
Db 624 CGAGCAGCGAACACGAGACTTGGCAATTTTATTAACACGATGTTGCTGACTATGACAAA 683
Qy 661 AAGCGTGAATTTCTTATCAGGATCAACGAGTCATCTGCTACTTTTAAAGAACGGGA 720
Db 684 CGAGAGATTTCCCGGAATGGAATAAACAAGCCATTTATCAGCTTATTTACGAACGGGG 743
Qy 721 GAATCTTCGATTCGCACCATTTTTCGCAAGAGCTTTCATCTGCTCTCTAGCTTAAAGTAAA 780
Db 744 GAAATCTCGATTCGACGATTTTTCGACACACTTCAAGAAACAGAGAACGAGACGA 803
Qy 781 GAAACCTTTCAAAAAGAAATTTAGCTTTCGCGGACACTTTTACAAATATGATCTATAGTGGCTTT 840
Db 804 GCTACATTTGAAAAGAACTGCTGAGCGGACACTTTTATTAATATGATTTACGTTCTCTTT 863
Qy 841 CCACAAACAAAAGAGGAGCTTATTCAGAAATAATTTTCGTTATATTCATTCAGACAAATGAC 900
Db 864 CTTAACCAAAAACGAGCGGATCCAGAAATAATTCGTTTATTTGAATGGGAAATAAAC 923
Qy 901 CCAGAAATGTTTGTCAAGTCGCAAAAGAGGAGCGGCTACCTATAATTTGATGCGCGCA 960
Db 924 CGCGAATATTTCAAGCGTGGCAAGATGGGAAGACTGGTTTCCGCTCGTTGATGCGGTG 983
Qy 961 ATGCGACAACTGAATCAAACTGGTTGATGATGACAACTCGTTTAAAGAAATGATTTACTGCTCT 1020
Db 984 ATGCGCCAGTTGCAAGAACTGGTGGTGCATCATCGACTAGAACTGTTTACGCTGACC 1043
Qy 1021 TTTTGTATTAATAATTTACATCGATTCGCTGTTGGGTGAAATAATACTTTTCAAAAATG 1080
Db 1044 TTTTAAACAAAGGATTTAGTTAGTGGCGGATTTGTCGAGAACTTTTCTTCAACTG 1103
Qy 1081 TTGATTCAGTATGATGCTGCAATAATATCGTGGCTGGCAATGCGCTTCAACAGGA 1140
Db 1104 CTGATGATTTCTGATCTCTGCGAGTCATATCGGGGCTGGCAATGCGGCTTCACTGGC 1163
Qy 1141 ACAGCGCTGCTGCTTATTTTCGGAATTTTAAATCCAAATTTCCAGTCAAAAATTTGAT 1200
Db 1164 ACAGTGGGGGCACTACTTTATGATCTTCAACGGAGCTGCTGCCACTGCAATTCCT 1223
Qy 1201 AATGACGCCAGTTTCATCAAAAATAATGTTTCCAGAACTTAAAGCAAGTGCACAAAGTAT 1260
Db 1224 TCCCTCGGAAATTCATTACCAATACTGCGCATGATTTGGCGAATCTGCTGCTTAT 1283
Qy 1261 ATTCAACCAAAATCTAATGAACGA 1286
Db 1284 CTCCATGCTCTCCATACACTGCCCCGA 1309

RESULT 8

US-08-781-986A-594
; Sequence 594, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: Hp Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A

Db 797 CATTTTATAGAGATTTTATTATGTTTAAATGACACAGTATCCTGAAACCTCATACCAAGC 856
Qy 861 TATTCAGAGAAAATTTGTTATATTCATATGAGCAAAATGACCAAGAAATGTTTGTCAAGTG 920
Db 857 TTTCAAACTAAATATGACACAGATAAATGTTGCGCAAAATGAAGCGGATTTTAAATGCATG 916
Qy 921 GCAAAAAGGGAGAGCGGTACCTATATATGATGCGCAATGCGACAATCGAATCAAAAC 980
Db 917 GTGCGAAGGGCAACACAGATTTCCAAATCATTTGATGCGACAAATATGGAATTTGACACAAAC 976
Qy 981 TGGTTGGATGACAAATCGCTTAAAGAAATGATTAATCGCTCTTTTTPAGTTAAAAATTTACA 1040
Db 977 TGGTTTATGCATATATCGAATGAGAAATGTTGTTGTCGCAATTTTAAACCAAGATTTATT 1036
Qy 1041 CATCGATTTGGCTGGGTGAAAAATACCTTCAAAAAATGTTGATGACTATGATGCTGC 1100
Db 1037 TATGATTTGGACATGGGAGAAAAATCTTTAGAAAAGCACCTTATTTGACTATGATGCAGC 1096
Qy 1101 CAATTAATATCGGTGGCTGCAATGGCTTCAACAGCAAGCGAGCTGTCCTTTATT 1160
Db 1097 ATCAAAATATTCATGATGGCAATGGCTTCTACAGTACGGATGCGATGCGGTATTT 1156
Qy 1161 TCGGATTTTAAATCCAAATATCCAGTCAAAAAATTTTGATATGACGGCCAGTTCCATCAA 1220
Db 1157 TAGAATGTTTAAATCAATTAAGACAGATGAAAGCTTTGATGCTAAAGCTTTGTATATCAA 1216
Qy 1221 AAAATATGTTCCAGAACTTAAAGCAAGTGCACAAAGTATATTCATCAACCAATCTAAT 1280
Db 1217 ACATATCTTCCGATTTTAAATCAAAATGATGCAAAATATTTGCAATGATACA --CAAG 1273
Qy 1281 GAACGAGCTTACAAACCAATATCATGATTTAGGAGAAATTTTCAAAACCCAT 1340
Db 1274 CAATGAGTCCAACTTTTGAACAGGGGATGAAATAGGTATGATTTATCCAAAGCAAT 1333
Qy 1341 TGTGATTTGATCATCAAGTAAACCAAAATTTTCTATATGATGAAGCG 1389
Db 1334 GGTAGATCATCAAGAAACGATACACAGTTTATGCTACATTTAAAGCG 1382

RESULT 10

US-10-724-972A-3359
; Sequence 3359, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PAT03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; PRIOR FILING DATE: 2003-12-01
; PRIOR FILING DATE: 2003-12-01
; PRIOR FILING DATE: 1999-11-29
; PRIOR FILING DATE: 1999-11-29
; PRIOR FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-11-08
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3359
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: S. epidermidis
US-10-724-972A-3359

Query Match 13.9%; Score 199; DB 7; Length 1380;
Best Local Similarity 58.9%; Pred. No. 1.3e-37;
Matches 362; Conservative 0; Mismatches 250; Indels 3; Gaps 1;
Qy 774 AAGTAAGAACCTTCAAAAAAGAAATAGCTTCGGCGAGCTTTTACAAATATGATCATAG 833
Db 759 AAATTAAGAACTTTTATACGTGAATTTTATAGAGATTTTATATGATTAATGAC 818

Qy 834 TGGTTTTCCACAAACAAAGAGGAGCTATTTCAAGAAAAATTTGTTTATATTTCAATGGAC 893
Db 819 CAATTATCCCGAAACAGCTCATGTTGCTTTTAAAGAAAAATACCAAAATTTGAATGGTC 878
Qy 894 AATGACCCAGAAATTTTGTCAAGTGGCAAAAAAGGGAGCGGTACCCCTATAATTGA 953
Db 879 TTATAATGAAGAGAAATTTTAAACCTGTGGNAAGATGGGAATCTAGTGTTCATATTTGA 938
Qy 954 TGGCGCAATCGCAACCTGAATCAAACTGGTTGGATGCACAATCGCTTAAAGAATGATTAC 1013
Db 939 TGCAGCAATGGAGAACTTAAACAACTGGATTTATGCAATAATCGCATGAGATGGTAGT 998
Qy 1014 TGCCTCTTTTATAGTTAAAAATTTACACATCGATGGCTTGGGTTGGGTTGAAAAATTTTCA 1073
Db 999 TTCTCAATTTTAACTAAAGATTTGTTTATTTGACTGGATTTGGGGTGGTCAATTTTCAA 1058
Qy 1074 AAAAATGTTGATGACTATGATGCTGCAATATATCGGTGGCTGCAATGGGCTGCTTC 1133
Db 1059 AAAAAATTAATAGATTTATGATGCACTTCAATGTTTCAAGGATGGCAGTGGTCAGCTTC 1118
Qy 1134 AACAGGAACGACGCTGTCCTTATTTTTCGGATTTTAAATCCAATTTTCAAGTCAAAAAA 1193
Db 1119 TACTGGAACAGATGCTGTACCACTTTTAGAATGTTTAAATCTATAGACAAGCGAGCG 1178
Qy 1194 ATTTGATAATGACGGCCAGTTTCATCAAAAAATATGTTTCCAGAACTTAAAGCAAGTCCACA 1253
Db 1179 TTTTGTATTAATGACAGATATATAAAATTTACATTTCAAGATTTAAATCAGGTAGATGC 1238
Qy 1254 AAGTATATTCATCAACCAAAATCTAATGAACGAAGCTTTACAAAGCAATATCATGTACA 1313
Db 1239 TAAGTATTTACAGCATCTCATAAATTCGAGCAACAAATAAAGGGGCAA ---GGTGTGA 1295
Qy 1314 TTTAGGAGAAATTTTCCAAACCCATTTGCTGATTTGCTATGCTCAAGTAAAAACAAACAT 1373
Db 1296 AATAGTAAAGACTATCTTAAACAAATGTTGATTCACAAAGAAAGTAGACAACGTTAAT 1355
Qy 1374 GTTTCTATATGAAGC 1388
Db 1356 GTCAGATTCAAAGC 1370

RESULT 11

US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 12.9%; Score 184.8; DB 3; Length 640681;
Best Local Similarity 54.2%; Pred. No. 7.4e-33;
Matches 465; Conservative 0; Mismatches 357; Indels 36; Gaps 3;
Qy 572 TTCTTTTAAACACACTATATAGTTCGCGGAAGAAACAGCCAGAGCGCTTAAATACCTTTTA 631
Db 331419 TTAATAAAAAATTTCTTCTGTTGGAGAAAAAGAGGCTATTAAATCGTTTAAAAAATTTT 331478

QY 632 TTGATCAAAACCTCAATCTATGAAATAAGCGTGAATTTTCCTTATCAGGATCAAAACGA 691
Db 331479 GTATATATAAATTAATGATTAATTTCTTAACAGAGATATCCCTTTTATGATGCTACTA 331538
QY 692 GTCAATCTGTCTACTTTTAAAGAACGGGAGAACTTTTCGATTCGACCACTTTGGCAAGAGC 751
Db 331539 GTATGCTGTCTCCATATTTATCAGCAGGAATAATCATCTCGATATTTGTCTTAAAGTGC 331598
QY 752 TTG-----CATCTGTGGCTCTAGCTTAAGTAAAGAAACCTTCAAAAAAGAA 798
Db 331599 TTTTAAAAACAAAAACAGCTCTCCATTAATTTCTTCTTACGCTCTCCITGGTTTGATC 331658
QY 799 TTAGCTTGGCGAGCTTTTACAAATATGATCTATAGTGGTTTCCACAAACAAAAAGAGAA 858
Db 331659 AGATATATGCGGTGAATTTTATACCAATTTATTAATTTGATTTCCAAAAATTTAGTAGAT 331718
QY 859 GCTATTCAAGAAAAATTTTCG-----TTATATTCAATGGACAAATGACCCGAAATGTTTG 913
Db 331719 CTGAATCATTTAGTAATGCGGAAAAAGAAATTCATTTGATATAATAATAAACAATTTTA 331778
QY 914 TCAAGTGGCAAAAGGGAGACGGGTACCTTAATTTGATGCGGCAATGGGCAACACTGA 973
Db 331779 ATGCTGGAAAGAGAAATACAGGTTTTCCTATAATAGATGACAGGAATGAGACAAATAA 331838
QY 974 ATCAAACTGGTTGGATGCACAACTCGCTTAAGAAATGATTACGCTCTTTTATGTTAAAA 1033
Db 331839 ACGAATCTAGGATGATGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 331898
QY 1034 ATTTACACATCGATTGGGTTGGGTTGAAAAATATCTTTTCAAAAAATGTTGATTGACTATG 1093
Db 331899 ATCTTTTGAATTAATGGGAGAGGGGAGAACTTTTATATCTAATTTAATCATGGAG 331958
QY 1094 ATGCTGCCAATAATATCGTGGCTGGCAATGGGCTGTTTCAAGAGGACGACCTGTCC 1153
Db 331959 ACTTAGCGCTGAATAATGAGGATGGCAATGGTCAAGCTGAGTGGGATGTTCTGTAC 332018
QY 1154 CTTATTTTCGGATTTTAAATCCAAATATCCAGTCAAAAAATTTGATAATGAGCGGCAGT 1213
Db 332019 CTTATTAAGAAATTTTAAATCCATTAATCAATCAAAAACTTTTATGATGATCGGTTAAT 332078
QY 1214 TCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGGCCAAAGTATATATTCATCAACCAA 1273
Db 332079 TTATAAGAAAGTTTATACCAAGATTAAGAAACGGTCAATCATATCATATCAACCAAC 332138
QY 1274 ATCTAATGAACGAGCCTTACAAAGCAATATCATGATTTAGGAGAAAAATTTATCAA 1333
Db 332139 AT-----GAAATGGTCAAAACAAAAAATTTTAAAAATAGATTATCCTA 332180
QY 1334 AACCCATTGCTGATTATGTCATCAAGTAAAGTAAACAAACAAATTTTCTATATGAACGAGCA 1393
Db 332181 ATCTTATTAATTAATATAGTGAAGAGCAAAAAACATCTTTATGCTATTCAAACAGCTC 332240
QY 1394 AAGAAATTCATCAAGAA 1411
Db 332241 GATTAAACCTCATAAAA 332258

RESULT 12

US-10-793-639-226
; Sequence 226, Application US/10793639
; Publication No. US20040199940A1
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/10793.639
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US/09/614,221A
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/142,981

; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 226
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-793-639-226

Query Match 9.6%; Score 137.2; DB 8; Length 1698;
Best Local Similarity 57.6%; Pred. No. 1.5e-22;
Matches 266; Conservative 0; Mismatches 193; Indels 3; Gaps 1;

QY 782 AAACCTTCAAAAAAGAAATAGCTTGGCGGACATTTTACACAAAATATGATGATGCGT 838
Db 1136 AAAATTTTCATCAAAAGAGTTGCAATGGAGAGATTTTACAGACATTTGATGCACTGGC 1195
QY 839 TTCCACAAACAAAGAGAGAGCTATTCAAGAAAAAATTTTCGTTATATTTCAATGGACAAATG 898
Db 1196 CATATACCTCAATGGGAATGCCCTTATCGATTGGACACTTTTAGATATAAAAAATGGAGAATA 1255
QY 899 ACCAGAAATGTTTTCGTCAGTGGCAAAAGGGAGAGCGGTACCTTATATTTGATGCGC 958
Db 1256 ACCCTGTAGCAATTTGAAAAATGCTGTCTGTTAATACAGGCATTTCCCATAGTCGATGCCA 1315
QY 959 CAATGGACAACTGAATCAAACTGGTTGGATGCACAACTCGCTTAAGAAATGATTACTGCT 1018
Db 1316 TAAAGAAAAATTTCTGTACAGAGCTATTTAATTAACAGATCTAGAAATGATCAGCTT 1375
QY 1019 CTTTTTTAGTTAAAAATTTTACACATCGATTGGCGTTGGGTGAAAAAATACTTTCAAAAAA 1078
Db 1376 CTTTTCTTTTAAAAAATTTAATTAATAGATTGGAGATGGGGGAAACGCTGTTTATGAAAC 1435
QY 1079 TGTGATGATGATGATGTCGCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAG 1138
Db 1436 ACTTGATGACGCTGCTGCTCTTCAAAATGTTGGTGGCTGGGCTTTTGTCTAGTACAG 1495
QY 1139 GAACGAGCGCTGCTGCTTATTTTCGGATTTTTCGATTTTAAATCCAAATATCCAGTCAAAAAATTTG 1198
Db 1496 GAATGATGCGCAACCAATATTTTAGAGTTTTTANTGATATACAGCAAAAAAATATG 1555
QY 1199 ATAATGACGGCCAGTTTCATCAAAAAAATATGTTCCAGAACTTA 1240
Db 1556 ACCACAAATGATATTTCGTCAAACAAATGGTTCCCGAAATTA 1597

RESULT 13

US-09-738-626-701
; Sequence 701, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 701

LENGTH: 1404
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-701

Query Match
Best Local Similarity 8.0%; Score 114.8; DB 3; Length 1404;
Matches 191; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 919 TGGCAAAAGGGAGACGGGGTACCTTATATGATGCGCAATGCGCAACTGAATCAA 978
DB 1003 TGGCGTCAGGAAAAACAGGAATTCGCTGTCGATGCGAGCATGCGAGAATTATGGGCC 1062

QY 979 ACTGTTGGATGCAATCGCTTAAAGATGATTCTCTCTTTTAAAGTAAATTTA 1038
DB 1063 ACCGGGTCAATGCAATCGCTGAGAATGGTAGTAGTCTTTTAAACAGAACTC 1122

QY 1039 CACATCGATTGGCGTTGGGGTGAAAAATATCTTTCAAAAAATTTGATTGACTATGATGCT 1098
DB 1123 CAGATCCATTGGCGTCATGGCGAAGATGGTTTGGGAACTCTCGTAGATGCTGATCCA 1182

QY 1099-GCCAATAATATCGGTGCGCAATGGCTGCTTCAACAGGAACGGAGCGCTGCTCCTTAT 1158
DB 1183 GCTTCTAATGCTTCAACTGGCAATGGCTGCGGGTAGCGAGATGACGCTTCGCTTAT 1242

QY 1159 TTTCGGATTTTAATCCAAATTCAGTCAAAAAATTTGATAATGACGGCCAGTTTCATC 1218
DB 1243 TTCCGTAATTTTAAATCCCGTCAACCCAGCAAAAAATTTGATCCAGATGAACCTTATAT 1302

QY 1219 AAAAAATATGTTCCAGAA 1236
DB 1303 CGTCTGGGTACCCGAA 1320

RESULT 14
US-09-738-626-1/c
Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match
Best Local Similarity 8.0%; Score 114.8; DB 3; Length 3309400;
Matches 191; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 919 TGGCAAAAGGGAGACGGGGTACCTTATATGATGCGCAATGCGCAACTGAATCAA 978

DB 642957 TGGCGTCAGGAAAAACAGGAATTCGCTGTCGATGCGAGCATGCGAGAAATATGGGCC 642898
QY 979 ACTGTTGGATGCACAATCGCTTAAAGATGATTACTGCTCTTTTATAGTTAAAAATTTA 1038
DB 642897 ACCGGGTCAATGCACAATCGCTGCAATGCTAGTAGTAGTTTAAACCAAGAACTC 642838
QY 1039 CACATCGATTGGCGTTGGGGTGAAAAATCTTTCAAAAAATGTTGATTGACTATGATGCT 1098
DB 642837 CAGATCCATTGGCGTCATGCGGAAGAAATGCTTTTGGGNAACCTCTCGTAGATGCTGATCCA 642778
QY 1099 GCCAATAATATCGGTGCGCAATGGCTGCTTCAACAGGAACGGACGCTGCTCCCTTAT 1158
DB 642777 GCTTCTAATGCTTCAACTGGCAATGGCTGCGGGTAGCGGAGATGACGCTTCGCTTAT 642718
QY 1159 TTTCGGATTTTAAATCCAAATTCAGTCAAAAAATTTGATAATGACGGCCAGTTTCATC 1218
DB 642717 TTTCGGATTTTAAATCCGTCACCCAGCGAAAAATTTGATCCAGATGAACCTTATAT 642658
QY 1219 AAAAAATATGTTCCAGAA 1236
DB 642657 CGTCTGGGTACCCGAA 642640

RESULT 15
US-09-938-842A-479
Sequence 479, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 479
LENGTH: 1839
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-479

Query Match
Best Local Similarity 7.3%; Score 104.2; DB 3; Length 1839;
Matches 280; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

QY 774 AAGTAAAGAAACCTTCAAAAAAGAAATAGCTTGGCGGACCTTTTCAATATGATCTATAG 833
DB 846 AAGTGCAGATCTTTTCTTAGGGAATCGTTTAAAGAGATATTCTCGGTATATATGTT 905
QY 834 TGGCTTTCCACAAACAAAAGAGGAGCTATTCAGAAAAATTTGTTATATATTCATGAC 893
DB 906 CAACTTCCGTTTACTCAGCAGCAATCGTTTGTAGTCATCTTCGGTTTTTCCCTTGGGA 965
QY 894 AATGACCCAGAAATGTTGTCAGTGCRAAAAGGGAGACGGGTACCTTATAATGA 953
DB 966 TGCTGATGTTGATAAGTTCAAGGCTGAGACCAAGGAGGACCGGTTATCCGTGGTGA 1025
QY 954 TGGCCCAATGCGCAACTGAATCAAACTGGTTGGATGCACAATCGCTTTAAGAATGATPAC 1013
DB 1026 TGGCGAATGAGAGCTTTGGGCTACCGGATGATGATTAACAGAAATAGAGTATGT 1085
QY 1014 TGCCTCTTTTATGTTAAAAATTTACATCGATGCGTTGGGGTGGGAAATACTTTCA 1073
DB 1086 TTCAAGCTTTGCTGTGAAGTTTCTTCTTCCATGGAAATGGGGAATGAAGTATTTCTG 1145

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OM nucleic - nucleic search, using sw model

Run on: December 20, 2005, 17:53:57 ; Search time 220 Seconds

(without alignments)
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Title: US-10-758-979-2

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Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

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- 2: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
- 5: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 7: /cgn2_6/prodata/1/pubpna/US12_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/1/pubpna/US13_NEW_PUB.seq.*
- 9: /cgn2_6/prodata/1/pubpna/US14_NEW_PUB.seq.*
- 10: /cgn2_6/prodata/1/pubpna/US15_NEW_PUB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52.8	3.7	1296	US-10-467-657-1889	Sequence 1889, Ap
2	52.8	3.7	1296	US-10-467-657-6127	Sequence 6127, Ap
C 3	43.6	3.0	156544	US-11-121-086-81	Sequence 81, Appl
C 4	39.6	2.8	1082144	US-11-117-187-211	Sequence 211, App
C 5	39.4	2.7	900	US-10-750-185-37504	Sequence 37504, A
C 6	37.6	2.6	3001	US-11-145-703-181	Sequence 181, App
C 7	37.6	2.6	3001	US-11-145-703-197	Sequence 197, App
C 8	37.6	2.6	161874	US-11-121-086-75	Sequence 75, Appl
C 9	37.2	2.6	649	US-10-750-185-27667	Sequence 27667, A
C 10	37.2	2.6	1947	US-10-750-185-51012	Sequence 51012, A
C 11	37.2	2.6	207835	US-11-121-086-39	Sequence 39, Appl
C 12	37.2	2.6	207835	US-11-121-086-40	Sequence 40, Appl
C 13	37.2	2.6	398287	US-10-995-561-13396	Sequence 13396, A
C 14	36.4	2.5	7943	US-10-995-561-13397	Sequence 13397, A
C 15	36.2	2.5	1227	US-10-750-185-45849	Sequence 45849, A
C 16	36	2.5	965	US-10-750-185-63340	Sequence 63340, A
C 17	36	2.5	110950	US-10-857-780-2	Sequence 2, Appli
C 18	35.6	2.5	611587	US-11-117-187-209	Sequence 209, App
C 19	35.4	2.5	2982	US-10-793-626-4028	Sequence 4028, Ap
C 20	35.4	2.5	3114	US-10-750-185-32681	Sequence 32681, A
C 21	35.4	2.5	142303	US-11-121-086-42	Sequence 42, Appl
C 22	35	2.4	1839	US-10-750-185-59311	Sequence 59311, A
C 23	35	2.4	134174	US-11-121-086-99	Sequence 99, Appl

C	24	34.8	2.4	1069	6	US-10-750-185-27770	Sequence 27770, A
	25	34.6	2.4	3543	6	US-10-793-626-3493	Sequence 3493, Ap
	26	34.6	2.4	193084	7	US-11-121-086-82	Sequence 82, Appl
	27	34.6	2.4	398287	6	US-10-995-561-13396	Sequence 13396, A
	28	34.6	2.4	611587	7	US-11-117-187-209	Sequence 209, App
C	29	34.4	2.4	926	6	US-10-750-185-60151	Sequence 60151, A
	30	34.4	2.4	1544	6	US-10-750-185-37654	Sequence 37654, A
C	31	34.4	2.4	3649	6	US-10-793-626-3725	Sequence 3725, Ap
	32	34.2	2.4	964	6	US-10-750-185-57739	Sequence 57739, A
C	33	34.2	2.4	1184	6	US-10-750-185-42797	Sequence 42797, A
	34	34.2	2.4	1794	6	US-10-750-185-32037	Sequence 32037, A
C	35	34.2	2.4	2017	6	US-10-750-185-37628	Sequence 37628, A
	36	34	2.4	3159	6	US-10-793-626-4112	Sequence 4112, Ap
	37	34	2.4	139054	7	US-11-121-086-96	Sequence 96, Appl
C	38	33.8	2.4	1011	6	US-10-750-185-26282	Sequence 26282, A
	39	33.8	2.4	1695	6	US-10-750-185-33604	Sequence 33604, A
C	40	33.6	2.3	2269	6	US-10-750-185-38234	Sequence 38234, A
	41	33.6	2.3	2690	6	US-10-750-185-57602	Sequence 57602, A
C	42	33.6	2.3	5855	7	US-11-108-528-27	Sequence 27, Appl
	43	33.6	2.3	12462	6	US-10-995-561-13395	Sequence 13395, A
C	44	33.6	2.3	65931	6	US-10-995-561-13254	Sequence 13254, A
	45	33.4	2.3	1508	7	US-11-086-904-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-467-657-1889
; Sequence 1889, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1889
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1889

Query Match	3.7%	Score 52.8	DB 6	Length 1296
Best Local Similarity	52.8%	Pred. No. 0.00045		
Matches 114	Conservative 0	Mismatches 102	Indels 0	Gaps 0
QY	919	TGGCAAAAGGGAGACGGGTACCTATAATGATCGCGCAATCGCAACTGAATCAA	978	
DB	904	TGGCAGCAGGCGCGGACCGGCATTCGATTCGATCGCGGATGCTGTTGCACAA	963	
QY	979	ACTGGTGGATGCACAATCGCTTAAGAATGATTACTGCCTCTTTTAAATAATTA	1038	
DB	964	ACCGCAGCTCCACCCGCCCTGAGCGCTTGAGCGCGGATTTTCTGCCACGTTTA	1023	
QY	1039	CACATCGATTGGCGTGGGTGAAATACTTTCAAAAATGTTGATTGACTATGATGCT	1098	
DB	1024	AACCTCCCGCCCGGAAGGCGAGATATGGTTTGGCCGGAGTCCGATTCGATCGG	1083	
QY	1099	GCCATAATATCGGTGGCTGGCAATGGCTGCTTCA	1134	
DB	1084	GAATCAACCAAGGCACTGGCGGCTTCCGCCCTCA	1119	

RESULT 2

US-10-467-657-6127
; Sequence 6127, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6127
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-6127

Query Match 3.7%; Score 52.8; DB 6; Length 1296;
Best Local Similarity 52.8%; Pred. No. 0.00045;
Matches 114; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy 919 TGGCAAAAGGGAGACGGGTACCTATATGATGCCGCAATGCACAACTGAATCAA 978
Db 904 TGGCAGAGGGCCGACGGCATTCGGATTATCGATGCCGGATGCGCTGTTGCACAAA 963

Qy 979 ACTGGTTGGATGACCAATCGTTAAGATGATTTACTGCCTCTTTTGTAGTTAAATTTA 1038
Db 964 ACCGGCAGCCTCCACCCGCCCTGAGACGCTTGAGCGCGATTTTCTGCCACGTTT 1023

Qy 1039 CACATCGATTGGCGTTGGGGTGAATAATACCTTCAAAAAATGTTGATTGACTATGATGCT 1098
Db 1024 AACTCCCCCGCGAAGCGAGATATGTTTCCCGCGAGCTGACCGATTCGATCGG 1083

Qy 1099 GCCAATAATATCGGTGGCTGGCAATGGCGTCTTCA 1134
Db 1084 GCAATCAACCAAGCAACTGGCGGCTTGCGGCCTCA 1119

RESULT 3
US-11-121-086-81/c
; Sequence 81, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 156544
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-81

Query Match 3.0%; Score 43.6; DB 7; Length 156544;
Best Local Similarity 48.4%; Pred. No. 0.83; Length 156544;
Matches 121; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

Qy 1184 AGTCAAAAAATTTGATAATGACGGCGGCTTCAATCAAAAAATATGTTCCAGAACTTAAGC 1243
Db 142633 AGACCCAAACATTGACAAATGCGACCTTAATACACTAAAGAACTTTTACACAGCAAGGA 142574

Qy 1244 AAGTGCCACAAAAGTATATTTCATCAACCAAAATCTAATGAACGAAGCCTTTACAAACGCAAT 1303
Db 142573 AACTATCAACAGAGTAAACAGGCAACTACAGAAATGTGAGAAAATATTTCGCAAACTATGT 142514

Qy 1304 ATCATGTACATTTTAGGAGAAAAATTTCCAAAAACCCATTGTCGATTATGCAATCAAGTAAAA 1363
Db 142513 ATCAGCAAAAGGTGTAATATCCAGAATCTATAAGAAACTTTAAGCAAAATTAACAAGCAAAA 142454

Qy 1364 AACAAACATTGTTTCTATATGAAGCAGCAAGAAATTCATCAAGAAATGAACAATCCAA 1423
Db 142453 AACAAACACATGAACAGACAAAATGGAAAAACGACATGAACAGATACTTCTCAAAAGAA 142394

Qy 1424 GGTTCATA 1433
Db 142393 GACATCAATA 142384

RESULT 4
US-11-117-187-211/c
; Sequence 211, Application US/11117187
; Publication No. US20050286560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPEHAEVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD-309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 211
; LENGTH: 1082144
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-11-117-187-211

Query Match 2.8%; Score 39.6; DB 7; Length 1082144;
Best Local Similarity 46.2%; Pred. No. 20;
Matches 132; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

Qy 1056 GGGTGAATAATCTTTCAAAAAATGTTGATTGACTATGATGCTGCCAATAATATCGGTGG 1115
Db 418107 GGTTCGAAATATTTTAAACAAAAGAGTTTATGATTTGGTAACTCTGTCAGTAAGCTGGATAT 418048

Qy 1116 CTGGCAATGGGCTGCTTCAACAGGAACGGACGCTGCTCCCTTATTTTCGGATTTTAAATCC 1175
Db 418047 GTTCAATATACGTGAGATGCACGAAAGAGCATCTTATTTAATGTAGTTAGTAATTA 417988

Qy 1176 AATTATCCAGTCAAAAAATTTTGATTAATGACGGCCAGTTTCATCAAAAAATATGTTCCAGA 1235
Db 417987 AAAATTACAGTAAAGACTAGTTTATTTATTTGTTTATTAATAAAGAAAGTTGTAAG 417928

Qy 1236 ACTTAAGCAAGTCCCAACAAAGATATTCATCAACCAATCTTAATGAACGAACCTTACA 1295
Db 417927 AATTATTGAAAACGCAAAAAGTTTAAAAATATTTAAAGAACCAATATTAAACGTTGACCAAAA 417868

Qy 1296 AACGCAATATCATGTACATTTAGGAGAAAAATTTATCCAAAACCCATT 1341
Db 417867 ARCCCAAGACCAATATCTATATTTTAAATTTTAAAGAAACCAAT 417822

RESULT 5
US-10-750-185-37504
; Sequence 37504, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard

```
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 37504
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Bovine 19866881386126
US-10-750-185-37504

Query Match          2.7%; Score 39.4; DB 6; Length 900;
Best Local Similarity 59.3%; Pred. No. 1;
Matches 67; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 772 TTAAGTAAAGAAACCTTCACAAAAGAAATTAGCTTGGCGGACTTTTACAAATATGATCTAT 831
Db 762 TCAAGTAGGGAACCTCCAAAACATCTAGCTTTATGCTCTTTTACTTTACGCCCTG 821

QY 832 AGTGGCTTTCCACACAAAAGAGGAGCTATTCAGAAAAAATTTGCTTATAT 884
Db 822 TGTTGTTTTCATGATAGTAGGCAAAACCTTTTGCAAAAGACTCTTTTAAAT 874

RESULT 6
US-11-145-703-181/c
; Sequence 181, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: 53.US16.DIV
; CURRENT APPLICATION NUMBER: US/11/145,703
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US/10/147,603
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 09/539,333
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: Patent.pm
; SEQ ID NO 181
; LENGTH: 3001
; TYPE: DNA
; ORGANISM: Homo Sapiens
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; FEATURE:
; NAME/KEY: allele
; LOCATION: 1501
; OTHER INFORMATION: 99-25869-182 : polymorphic base A or C
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1482..1500
; OTHER INFORMATION: 99-25869-182.mis1
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1502..1521
; OTHER INFORMATION: 99-25869-182.mis2, complement
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1320..1340
; OTHER INFORMATION: upstream amplification primer
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1849..1868
; OTHER INFORMATION: downstream amplification primer, complement
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-25869-182 probe
US-11-145-703-181

Query Match          2.6%; Score 37.6; DB 7; Length 3001;
Best Local Similarity 51.8%; Pred. No. 4.9;
Matches 85; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1226 ATGTTCCAGAACTTAAGCAAGTGCCACAAAAGTATATTCATCAACCAAAATCTAATGAACG 1285
Db 1542 ATTTTACAGAAATGATGGTGATATTTAAACACATAAATAATKTAACATTTATGCTAAAT 1483

QY 1286 AGCCCTTACAAACGCAATATCATGTACATTTAGGAGAAATTTATCCAAAACCCATTGTG 1345
Db 1482 GATTTTAATAAAGTTAATAATAAATAATAAATAAAGAGAAATGATTATGACCCCAATTAAT 1423

QY 1346 ATTATGCATCAAGTAAAAAACAACATTTGTTCTATATGAACG 1389
Db 1422 AGTGTAGTATCATGTAAAAAGAACTGTTTATGTTCTACTAGAG 1379

RESULT 7
US-11-145-703-197/c
; Sequence 197, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: 53.US16.DIV
; CURRENT APPLICATION NUMBER: US/11/145,703
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US/10/147,603
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 09/539,333
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
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; APPLICANT: BATES, Stephen
; APPLICANT: FANIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51012
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Bovine 19866881060052
US-10-750-185-51012

Query Match          2.6%; Score 37.2; DB 6; Length 1947;
Best Local Similarity 47.1%; Pred. No. 5.2;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 1149 TGTCCCTTTATTCGGATTTTAAATCCAAATTCAGTCACAAATAATTTGATGACGG 1208
Db 1564 TTTGCTTTAACAAGAAATAGCAATTTAGTGTTTAGAGTAAATGAATACCTTTTGTACTT 1623

Qy 1209 CCAGTTCAATAAATAATGTTCCAGAACTTAAGCAAGTGCACAAAAAGTATATTCATCA 1268
Db 1624 ACTGTGCTGATGAAGAAATAGGAAGAAAGAAACCAATTAATTAATATATATAAAA 1683

Qy 1269 ACCAAATCTAATGAACGAAGCCTTACAAACGCAATATCATGTGACATTTAGGAGAAATTA 1328
Db 1684 ACAATCAACTATATATATATATATATATATATATATATATATATATATATATATATA 1743

Qy 1329 TCCAAACCCATTTGCGATTTATGCAATCAAGTAAAGTAAACAAACATTTGTTTCTATATGA 1388
Db 1744 AATTGCTCATATGTCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1803

Qy 1389 GA 1390
Db 1804 GA 1805

RESULT 11
US-11-121-086-39/c
; Sequence 39, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
; LENGTH: 207835
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-39

Query Match          2.6%; Score 37.2; DB 7; Length 207835;
Best Local Similarity 47.1%; Pred. No. 40;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 1171 AATCCAAATTCAGTCACAAATAATTTGATAATGACGCCAGTTCATCAAAAAAATATGTT 1230
Db 185580 AAGCAAAATGCAATTAATAAACAAGATAAATAGCTGGACCAATTAACCTAAAGAGCTTTT 185521

Qy 1231 CCAGAACTTAAGCAAGTGCACAAAGATATATTCATCAACCAAAATCTTAATGACGAAGCC 1290
Db 185520 GCATGGCAAAAGGAACAGTCAGCAAGTAAACAGACAAACCCACAGAGTGGAGAAAATCT 185461

Qy 1291 TTACAAACGCAATATCATGTACATTTAGGAGAAAATTTCCAAAACCCATTTGTCGATTAT 1350
Db 185460 TCACAATCTATACATCTGCACAAAGACTTAATAACAAGAAATCTGCAATGAACCTCAACAA 185401

Qy 1351 GCATCAAGTAAATAAACAACATTTGTTCTATATGAAGCGAGCAAAAGAAATTCATCAAGAA 1410
Db 185400 TCAGTAAGAAAAAACAACAATCCCAACCAAAAGAGTGGGCTAGGACATGAATAGTCAA 185341

Qy 1411 AT 1412
Db 185340 TT 185339

RESULT 13
US-10-995-561-13396/c
; Sequence 13396, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702

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Qy 1291 TTACAAACGCAATATCATGTACATTTAGGAGAAAAATTTCCAAAACCCATTTGTCGATTAT 1350
Db 185460 TCACAATCTATACATCTGCACAAAGACTTAATAACAAGAAATCTGCAATGAACCTCAACAA 185401

Qy 1351 GCATCAAGTAAATAAACAACATTTGTTCTATATGAAGCGAGCAAAAGAAATTCATCAAGAA 1410
Db 185400 TCAGTAAGAAAAAACAACAATCCCAACCAAAAGAGTGGGCTAGGACATGAATAGTCAA 185341

Qy 1411 AT 1412
Db 185340 TT 185339

RESULT 12
US-11-121-086-40/c
; Sequence 40, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40
; LENGTH: 207835
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-40

Query Match          2.6%; Score 37.2; DB 7; Length 207835;
Best Local Similarity 47.1%; Pred. No. 40;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 1171 AATCCAAATTCAGTCACAAATAATTTGATAATGACGCCAGTTCATCAAAAAAATATGTT 1230
Db 185580 AAGCAAAATGCAATTAATAAACAAGATAAATAGCTGGACCAATTAACCTAAAGAGCTTTT 185521

Qy 1231 CCAGAACTTAAGCAAGTGCACAAAGATATATTCATCAACCAAAATCTTAATGACGAAGCC 1290
Db 185520 GCATGGCAAAAGGAACAGTCAGCAAGTAAACAGACAAACCCACAGAGTGGAGAAAATCT 185461

Qy 1291 TTACAAACGCAATATCATGTACATTTAGGAGAAAATTTCCAAAACCCATTTGTCGATTAT 1350
Db 185460 TCACAATCTATACATCTGCACAAAGACTTAATAACAAGAAATCTGCAATGAACCTCAACAA 185401

Qy 1351 GCATCAAGTAAATAAACAACATTTGTTCTATATGAAGCGAGCAAAAGAAATTCATCAAGAA 1410
Db 185400 TCAGTAAGAAAAAACAACAATCCCAACCAAAAGAGTGGGCTAGGACATGAATAGTCAA 185341

Qy 1411 AT 1412
Db 185340 TT 185339

RESULT 13
US-10-995-561-13396/c
; Sequence 13396, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13396
; LENGTH: 398287
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(398287)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13396

Query Match          2.6%; Score 37.2; DB 6; Length 398287;
Best Local Similarity 47.1%; Pred. No. 53;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 1191 AAAATTTGATATGACGGCCAGTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCC 1250
Db 51285 AAAATTGACAAATGGGCTCCAGTTAAACTAAAGAGCTTCTGCACAGCAAAAGGAATATC 51226

Qy 1251 ACAAAGTATATTATCAACCAATCTTAATGAACGAAGCCCTTACAAACGGCAATATCATGT 1310
Db 51225 ACCAGAGTGAACAGGCAACCTTACAGAATGGGAGAAAAATTTTGGCAATCTATCCATCTGAC 51166

Qy 1311 ACATTTAGGAGAAAAATATTCCAAAAACCATTTGTCGATTATGTCATCAAGTAAAAACAAAC 1370
Db 51165 AAAGGGCTAATATCCAGATCTACAGGAATTTAAACAAATTTACAGAAAAAACAAG 51106

Qy 1371 ATGTTTTCTATATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAATCCAAGTTTCA 1430
Db 51105 ACAACTCCATCAAAAAGTAGTGAAGGATATGAACAGCAATTTATCAAAAGNAGACATTT 51046

Qy 1431 AT 1432
Db 51045 AT 51044

RESULT 14
US-10-995-561-13397/c
; Sequence 13397, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13397
; LENGTH: 7943
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13397

Query Match          2.5%; Score 36.4; DB 6; Length 7943;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 91; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 1190 AAAAATTTGATATGACGGCCAGTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCC 1249
Db 4024 AAAAACTGACAAATGGGATCTTAATTAACCTAAAGAGCTTCTGCACAGCAAAAGGAATAT 3965

Qy 1250 CAAAAAGTATATTATCAACCAATCTTAATGAACGAAGCCCTTACAAACGCAATATCATG 1309
Db 3964 CAGCAGAGTAAAGAGATAA CCTACAGATGGGAGAAAATATTATCAAACTATGTATCTCA 3905

Qy 1310 TACATTTAGGAGAAAAATTTATCCAAAAACCCATTTGCGATTATGTCATCAAGTAAAAACAAA 1369
Db 3904 CAAAGGTTAATATCCAGAACTTATAGGGAATTTAAACACATGTATCAAGCAAAAAACAAA 3845

Qy 1370 CA 1371
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Db 3844 CA 3843

RESULT 15
US-10-750-185-45849/c
; Sequence 45849, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45849
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Bovine 19866881281641
US-10-750-185-45849

Query Match          2.5%; Score 36.2; DB 6; Length 1227;
Best Local Similarity 48.3%; Pred. No. 7.6;
Matches 101; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Qy 1071 TCAAAAAATGTTGATTGACTATGCTGCCAATAATATCGTGGCTGGCAATGGGCTGC 1130
Db 281 TCAATGTAACCAACATCATCATATTACTATAAATAAAATTTAAATTTAAGATAACATTC 222

Qy 1131 TTCAACAGGAAACGGACGCTGCCCTTATTTTCGGATTTTAAATCCAAATTTATCCAGTCAA 1190
Db 221 TCCCATATGCTTGAATTTTCTCTTATTCTTAAATTTTGAACCTTTTATGACAGTTA 162

Qy 1191 ARAATTTGATAATGACGGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAAGCAAGTGCC 1250
Db 161 ACAGTGTGAAACATCAAAACATTCCTCCAGTAAAAGATACACAAACATACCCTTAAT 102

Qy 1251 ACAAAGTATATTTCATCAACCAAAATCTAA 1279
Db 101 TCAAGGCATGAATACCTAGATATCAAA 73

Search completed: December 20, 2005, 22:14:16
Job time : 224 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2005, 14:07:11 : Search time 944 Seconds
(without alignments)
10124.120 Million cell updates/sec

Title: US-10-758-979-2
Perfect score: 1434
Sequence: 1 atgaagaagagtaatatggtt.....acaatccaaggtttcaataa 1434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004as.*
13: geneseqn2004bs.*
14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1434	100.0	1434	ADJ33289	Adj33289 Enterococ
2	1434	100.0	2267	ADJ33288	Adj33288 Enterococ
3	1432.8	99.9	5277	AAJ13199	Aax13199 Enterococ
4	1432.8	99.9	5277	ABS98994	Ab98994 Enterococ
5	942	65.7	966	ADH83427	Adh83427 Enterococ
6	597	41.6	609	ADH83428	Adh83428 Enterococ
7	526.4	36.7	2460	ABQ70791	Abq70791 Listeria
8	518.4	36.2	110000	ABQ69245_06	Continuation (7 of
9	518.4	36.2	110000	ABQ67197_05	Continuation (6 of
10	516.8	36.0	110000	ABA03041_06	Continuation (7 of
11	416.8	29.1	1451	ABQ68877	Abq68877 Listeria
12	396.2	27.6	1440	ABN70089	Abn70089 Streptoco
13	212.2	14.8	1446	ADF03864	Adf03864 Bacterial
14	206.2	14.4	1389	ACF74095	Acf74095 Staphyloc
15	206.2	14.4	1393	AAV74905	Aav74905 Staphyloc
16	203.4	14.2	1608	ADA29102	Ada29102 DNA encod
17	201.4	14.0	5024	AAQ55139	Aaq55139 Staphyloc
18	201.4	14.0	5024	ABZ77355	Abz77355 Nucleotid
19	201.4	14.0	5024	AAJ51843	Aaj51843 Staphyloc

20	199	13.9	1380	6	ABN93166	Abn93166 Staphyloc
21	199	13.9	1380	13	ADS04064	Ads04064 Staphyloc
22	184.8	12.9	110000	6	ABA92787_3	Continuation (4 of
23	157.8	11.0	110000	14	AE339175_02	Continuation (3 of
24	157.8	11.0	110000	14	AE339175_03	Continuation (4 of
25	157.8	11.0	194588	14	AE335717	Aeb35717 L. pneumo
26	156.4	10.9	184951	14	AE342739	Aeb42739 L. pneumo
27	156.4	10.9	185021	14	AE339169	Aeb39169 L. pneumo
28	154.6	10.8	110000	14	AE342739	Continuation (3 of
29	117.4	8.2	1248	11	ABD00369_02	Abd00369 Klebsiell
30	114.8	8.0	1404	5	AAH65666	Aah65666 C. glutami
31	114.8	8.0	1428	8	ACA00095	Aca00095 C. glutami
32	114.8	8.0	349980	5	AAH68525	Aah68525 C. glutami
33	114.8	8.0	349980	5	AAH68526	Aah68526 C. glutami
34	109.8	7.7	1638	11	ABD15391	Abd15391 Pseudomon
35	109.8	7.7	2514	11	ABD15538	Abd15538 Pseudomon
36	104.2	7.3	978	3	AAH37888	Aac37888 Arabidops
37	104.2	7.3	1839	3	AAC48461	Aac48461 Arabidops
38	104.2	7.3	1839	6	ABZ12674	Abz12674 Arabidops
39	104.2	7.3	2188	3	AAC37009	Aac37009 Arabidops
40	102.6	7.2	2200	2	AAT16309	Aat16309 Arabidops
41	101.6	7.1	535	8	ABZ56081	Abz56081 Aspergill
42	99.2	6.9	1803	13	ADX11011	Adx11011 Plant ful
43	99.2	6.9	2264	13	ADX36310	Adx36310 Plant ful
44	99.2	6.9	2533	13	ADX64757	Adx64757 Plant ful
45	99.2	6.9	2649	13	ADX49572	Adx49572 Plant ful

ALIGNMENTS

RESULT 1
ADJ33289
ID ADJ33289 standard; DNA; 1434 BP.
XX
AC ADJ33289;
XX
DT 22-APR-2004 (first entry)
XX
DE Enterococcus faecalis photolase encoding DNA SEQ ID NO:2.
XX
KW Enterococcal; virulence factor; drug discovery; vaccine;
KW microbial infection; antimicrobial; bacterial pathogenesis; photolase;
KW enzyme; gene; ds.
XX
OS Enterococcus faecalis.
XX
FH Key Location/Qualifiers
FT CDS 1..1434
FT /*tag= a
FT /product= "photolase"
XX
PN WO2003056295-A2.
XX
PD 10-JUL-2003.
XX
PF 18-JUL-2002; 2002WO-US022979.
XX
PR 18-JUL-2001; 2001US-0306212P.
XX
PA (GENO) GEN HOSPITAL CORP.
XX
PI Ausubel FM, Garsin D, Mylonakis EE, Calderwood SB, Sifri CD;
XX
DR WPI; 2003-559298/52.
XX
PT P-PSDB; ADJ33243.
XX
PT New polypeptide, useful for preparing a composition for treating or
PT preventing a microbial infection.
XX
PS Claim 2; SEQ ID NO 2; 140pp; English.
XX
CC The present invention describes Enterococcal virulence factors (I), which

CC can act as targets for drug discovery. Also described: (1) an isolated
CC nucleic acid encoding (I); (2) a vector or host cell comprising the
CC nucleic acid; (3) a method of screening a compound for effectiveness as
CC an antagonist of (I); (4) a composition comprising the antagonist
CC compound; (5) a method of screening a compound for effectiveness in
CC altering expression of (I); (6) a method of treating an individual;
CC vaccine composition comprising the polypeptide and a vehicle; and (8) a
CC method of treating or preventing a microbial infection. (I) is useful for
CC preparing a composition having antimicrobial activity for treating or
CC preventing a bacterial pathogenesis e.g. microbial infection. The present
CC sequence encodes an Enterococcus photolysase, which is used in the
CC exemplification of the present invention.

XX
SQ Sequence 1434 BP; 496 A; 261 C; 269 G; 408 T; 0 U; 0 Other;

Query Match 100.0%; Score 1434; DB 10; Length 1434;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAGAGCTAAATGGTTAGACGCTGATTACGATTACAGGATTAAGCAATTAGCA 60
Db 1 ATGAAGAGCTAAATGGTTAGACGCTGATTACGATTACAGGATTAAGCAATTAGCA 60
Qy 61 CACGGCTTACAAAATCTCGACGCTGATCAATGATTTATTTCCAAATGAATCCTCAA 120
Db 61 CACGGCTTACAAAATCTCGACGCTGATCAATGATTTATTTCCAAATGAATCCTCAA 120
Qy 121 CAATTTATTCAGAAAGTGCTAATCAATAGCGTTTTTTTGAAGCTTAGCGTCTGTTCAA 180
Db 121 CAATTTATTCAGAAAGTGCTAATCAATAGCGTTTTTTTGAAGCTTAGCGTCTGTTCAA 180
Qy 181 GAACGATCGATCAAGAGGCGACATTTACAAATCATGCTCGCGAACCATTAGATTATTT 240
Db 181 GAACGATCGATCAAGAGGCGACATTTACAAATCATGCTCGCGAACCATTAGATTATTT 240
Qy 241 TCAGCTTTGAAACGCAATATACCGGATTTGGCAGGCCATTTATTTTAAAGATACATGTT 300
Db 241 TCAGCTTTGAAACGCAATATACCGGATTTGGCAGGCCATTTATTTTAAAGATACATGTT 300
Qy 301 GGCTTTGGGGCAAGCGGGACAGCAAGCTATGCGTTTTTTTGAAGAAATAATATTTCAG 360
Db 301 GGCTTTGGGGCAAGCGGGACAGCAAGCTATGCGTTTTTTTGAAGAAATAATATTTCAG 360
Qy 361 TCTTCTCTTTTCAAGATGCTATTTTCGTCGCTCTCAAGAAATTAAGACGATGCG 420
Db 361 TCTTCTCTTTTCAAGATGCTATTTTCGTCGCTCTCAAGAAATTAAGACGATGCG 420
Qy 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAATGGAAGAGCGCCCTAAAGAAACA 480
Db 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAATGGAAGAGCGCCCTAAAGAAACA 480
Qy 481 CCGATTCTGTTTCTTATACAGCTGAAATAATTTTATGTCGCTCTTTTTCCAGAAGAG 540
Db 481 CCGATTCTGTTTCTTATACAGCTGAAATAATTTTATGTCGCTCTTTTTCCAGAAGAG 540
Qy 541 GAACGAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAACACACTATAGTGTGCGGAA 600
Db 541 GAACGAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAACACACTATAGTGTGCGGAA 600
Qy 601 GAAACAGCCAGAGCGCTTAAATACCTTTTATTCATCAAAAACCTTCAATCCTATGAAAT 660
Db 601 GAAACAGCCAGAGCGCTTAAATACCTTTTATTCATCAAAAACCTTCAATCCTATGAAAT 660
Qy 661 AAGCGTGATTTTCTTATCAGGATCAACAGAGCTTCTGTCCTTTTAAAGAACGGGA 720
Db 661 AAGCGTGATTTTCTTATCAGGATCAACAGAGCTTCTGTCCTTTTAAAGAACGGGA 720
Qy 721 GAACCTTCGATTCCGACCATTTGGCAAGAGCTTCTGTCCTTTTAAAGTAAGTAA 780
Db 721 GAACCTTCGATTCCGACCATTTGGCAAGAGCTTCTGTCCTTTTAAAGTAAGTAA 780
Qy 781 GAAACCTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTAGTGCCTTT 840
Db 781 GAAACCTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTAGTGCCTTT 840

Db 781 GAAACCTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAGTGCCTTT 840
Qy 841 CCACACAAAAGAGAGAGCTATTCAAGAAAATTTTCGTTATATTCAATGGACAAATGAC 900
Db 841 CCACACAAAAGAGAGAGCTATTCAAGAAAATTTTCGTTATATTCAATGGACAAATGAC 900
Qy 901 CCAGAAATGTTTCTCAAGTGGCAAAAAGGGAGACGGGTACCTATAATTGATGCGCA 960
Db 901 CCAGAAATGTTTCTCAAGTGGCAAAAAGGGAGACGGGTACCTATAATTGATGCGCA 960
Qy 961 ATGCGCAATCGAATCAAACTGGTTCGATGCAATCGCTTAAGAAATGATCTAGTGCCTCT 1020
Db 961 ATGCGCAATCGAATCAAACTGGTTCGATGCAATCGCTTAAGAAATGATCTAGTGCCTCT 1020
Qy 1021 TTTTATGTTAAAAATTTTACACATCGATTGGCGTTGGGGTGAATAATCTTTCAAAAATG 1080
Db 1021 TTTTATGTTAAAAATTTTACACATCGATTGGCGTTGGGGTGAATAATCTTTCAAAAATG 1080
Qy 1081 TTGATTGACTATGATGCTGCAATAATATCGGTGGCTGGCAATGGCTGCTTCAACAGGA 1140
Db 1081 TTGATTGACTATGATGCTGCAATAATATCGGTGGCTGGCAATGGCTGCTTCAACAGGA 1140
Qy 1141 ACGGACGCTGCTCCTTTATTTTCGGATTTTAAATCCAAATATCCAGTCAAAAAATTTGAT 1200
Db 1141 ACGGACGCTGCTCCTTTATTTTCGGATTTTAAATCCAAATATCCAGTCAAAAAATTTGAT 1200
Qy 1201 AATGACGGCGAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCACAAAAATGAT 1260
Db 1201 AATGACGGCGAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCACAAAAATGAT 1260
Qy 1261 ATTCAATCAACCAATCTAATGAACGAAGCTTTACAAACGCAATATCATGTACATTTAGGA 1320
Db 1261 ATTCAATCAACCAATCTAATGAACGAAGCTTTACAAACGCAATATCATGTACATTTAGGA 1320
Qy 1321 GAAATATTCCAAAAACCCATTGTCGATTATGCAATCAAGTAAAAAACAACATTTGTTCTA 1380
Db 1321 GAAATATTCCAAAAACCCATTGTCGATTATGCAATCAAGTAAAAAACAACATTTGTTCTA 1380
Qy 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAAATCCAGGTTTCAATAA 1434
Db 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAAATCCAGGTTTCAATAA 1434

RESULT 2

ADJ33288
ID ADJ33288 standard; DNA; 2267 BP.

XX AC ADJ33288;

XX AC (first entry)

XX 22-APR-2004

XX Enterococcus faecalis photolysase encoding DNA SEQ ID NO:1.
DE DE
XX Enterococcus; virulence factor; drug discovery; vaccine;
KW microbial infection; antimicrobial; bacterial pathogenesis; photolysase;
KW enzyme; gene; ds.
XX OS Enterococcus faecalis.

XX Key Location/Qualifiers
FH CDS 568..2001
FT /*tag= a
FT /product= "photolysase"

XX WO2003056295-A2.

XX 10-JUL-2003.

XX 18-JUL-2002; 2002WO-US022979.

XX 18-JUL-2001; 2001US-0306212P.

XX (GEO) GEN HOSPITAL CORP.

XX Ausubel FM, Garstin D, Mylonakis EE, Calderwood SB, Sifri CD;
XX WPI; 2003-559298/52.
DR P-PSDB; ADJ33243.
XX New polypeptide, useful for preparing a composition for treating or
PT preventing a microbial infection.
XX Disclosure; SEQ ID NO 1; 140pp; English.
PS The present invention describes Enterococcal virulence factors (I), which
CC can act as targets for drug discovery. Also described: (1) an isolated
CC nucleic acid encoding (I); (2) a vector or host cell comprising the
CC nucleic acid; (3) a method of screening a compound for effectiveness as
CC an antagonist of (I); (4) a composition comprising the antagonist
CC compound; (5) a method of screening a compound for effectiveness in
CC altering expression of (I); (6) a method of treating an individual;
CC vaccine composition comprising the polypeptide and a vehicle; and (8) a
CC method of treating or preventing a microbial infection. (I) is useful for
CC preparing a composition having antimicrobial activity for treating or
CC preventing a bacterial pathogenesis e.g. microbial infection. The present
CC sequence encodes an Enterococcal photolase, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 2267 BP; 801 A; 387 C; 416 G; 663 T; 0 U; 0 Other;
Query Match 100.0%; Score 1434; DB 10; Length 2267;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAAGAGTAAATGGTTTAGCGTGAATTTACGATTACAGGATAAAGCATTAGCA 60
DB 568 ATGAAAGAGTAAATGGTTTAGCGTGAATTTACGATTACAGGATAAAGCATTAGCA 627
QY 61 CACGGGTTACAAATCTCGAGTGAATTTGATTTTATTTATTCGAATGATCTCTCAA 120
DB 628 CACGGGTTACAAATCTCGAGTGAATTTGATTTTATTTATTCGAATGATCTCTCAA 687
QY 121 CAATTTATTCAGAAAGTCTAATCAATACGCTTTTTCGAAAGCTTAGCCCTCGTTCAA 180
DB 688 CAATTTATTCAGAAAGTCTAATCAATACGCTTTTTCGAAAGCTTAGCCCTCGTTCAA 747
QY 181 GAAACGAATCGATCAAGAGGACACATTTACAAATCATGGTCGGCGAACCATTAGATTATTT 240
DB 748 GAAACGAATCGATCAAGAGGACACATTTACAAATCATGGTCGGCGAACCATTAGATTATTT 807
QY 241 TCACGTTTGAACCGCAATTTACCGGATTCGGAGCCATTTATTTAATGAAGATCTTGT 300
DB 808 TCACGTTTGAACCGCAATTTACCGGATTCGGAGCCATTTATTTAATGAAGATCTTGT 867
QY 301 GGCTTTGGGCGCAAGCGGACAGCAAGCTATGCGCTTTTTCGAAAGAAATATATTTCAG 360
DB 868 GGCTTTGGGCGCAAGCGGACAGCAAGCTATGCGCTTTTTCGAAAGAAATATATTTCAG 927
QY 361 TCTTTCTCTTTTCAAGATGCTATTTTCATGGCTCTGAAGAAATTAAGAAAGACGATGCG 420
DB 928 TCTTTCTCTTTTCAAGATGCTATTTTCATGGCTCTGAAGAAATTAAGAAAGACGATGCG 987
QY 421 AGCAAGTACCAAGTGTTTAGCGCTATTACATTAATGAAGAGCGGCTTAAGAAACA 480
DB 988 AGCAAGTACCAAGTGTTTAGCGCTATTACATTAATGAAGAGCGGCTTAAGAAACA 1047
QY 481 CCGATTCCGTTTCTTATACAGCTGAAAAATTTTGTAGTCGCTCTTTTCAGAAAGAG 540
DB 1048 CCGATTCCGTTTCTTATACAGCTGAAAAATTTTGTAGTCGCTCTTTTCAGAAAGAG 1107
QY 541 GAAGACGCTTTATCGTGAACAGATTGGAGGATTTCTTTTAAACACATATATGTGCGCGAA 600
DB 1108 GAAGACGCTTTATCGTGAACAGATTGGAGGATTTCTTTTAAACACATATATGTGCGCGAA 1167
QY 601 GAAACAGCCAGAGGCGCTTAAATACATTTTATGTATCAAAAACCTTCAATCTATGAAT 660

DB 1168 GAAACAGCCAGAGGCGCTTAAATACATTTTATGTATCAAAAACCTTCAATCTATGAAT 1227
QY 661 AAGCGTGAATTTCTTATCAGGATCAAAACGAGTCATCTGTCTACTTTTAAAGAACGGGA 720
DB 1228 AAGCGTGAATTTCTTATCAGGATCAAAACGAGTCATCTGTCTACTTTTAAAGAACGGGA 1287
QY 721 GAACTTTTCGATTCGCACCATTTGGCAAGAGCTTGTGCCTTCTAGCTTAAGTAA 780
DB 1288 GAACTTTTCGATTCGCACCATTTGGCAAGAGCTTGTGCCTTCTAGCTTAAGTAA 1347
QY 781 GAAACCTTTCAAAAAGAAATTTAGCTTGGCGGACATTTTACATATATGATCTAGTGGCTT 840
DB 1348 GAAACCTTTCAAAAAGAAATTTAGCTTGGCGGACATTTTACATATATGATCTAGTGGCTT 1407
QY 841 CCACAAACAAAAGAGGAGGCTATTCAAGAAAATTTTCGTTATATTCAATGGACAAATGAC 900
DB 1408 CCACAAACAAAAGAGGAGGCTATTCAAGAAAATTTTCGTTATATTCAATGGACAAATGAC 1467
QY 901 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGTACCTATAATTTGATGCGGCA 960
DB 1468 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGTACCTATAATTTGATGCGGCA 1527
QY 961 ATGCGACAACTGAATCAAACTGGTTGGATGCACAATCGCTTAAGAAATGATTTGCTCT 1020
DB 1528 ATGCGACAACTGAATCAAACTGGTTGGATGCACAATCGCTTAAGAAATGATTTGCTCT 1587
QY 1021 TTTTGTAGTAAAAATTTTACACATCGATTTGGGCTGGGCTGAAAAATATCTTTCAAAAATG 1080
DB 1588 TTTTGTAGTAAAAATTTTACACATCGATTTGGGCTGGGCTGAAAAATATCTTTCAAAAATG 1647
QY 1081 TTGATTGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA 1140
DB 1648 TTGATTGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA 1707
QY 1141 ACGGACGCTGCTCTTATTTTCGGATTTTAAATCCAAATATTCAGTCAAAAAATTTGAT 1200
DB 1708 ACGGACGCTGCTCTTATTTTCGGATTTTAAATCCAAATATTCAGTCAAAAAATTTGAT 1767
QY 1201 AATGACGGCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTCCCAAAAGTAT 1260
DB 1768 AATGACGGCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTCCCAAAAGTAT 1827
QY 1261 ATTCAATCAACCAATCTAATGAACGAGCTTTACAAACGCAATATCATGTATATTAGGA 1320
DB 1828 ATTCAATCAACCAATCTAATGAACGAGCTTTACAAACGCAATATCATGTATATTAGGA 1887
QY 1321 GAAATTTATCCAAACCCATTTGTGATTTATGATCAAGTAAACAAACATTTGTTCTA 1380
DB 1888 GAAATTTATCCAAACCCATTTGTGATTTATGATCAAGTAAACAAACATTTGTTCTA 1947
QY 1381 TATGAGCGGAGCAAGAAATTTTCATCAAGAAATGAACATCCAGGTTTCAATAA 1434
DB 1948 TATGAGCGGAGCAAGAAATTTTCATCAAGAAATGAACATCCAGGTTTCAATAA 2001
RESULT 3
AA13199
ID AA13199 standard; DNA; 5277 BP.
XX
AC AA13199;
XX
DT 19-MAR-1999 (first entry)
XX
DE Enterococcus faecalis genome contig SEQ ID NO:262.
XX
KW Enterococcus faecalis; contig; detection; Enterococcal infection;
KW vaccine; attenuation; computer readable medium; ds.
XX
OS Enterococcus faecalis.
XX
PN WO980555-A2.
XX
PD 12-NOV-1998.

KW Computer readable medium: Enterococcus faecalis; microbe; growth;
 KW pathogenicity; vaccine; resistance; Enterococcal infection; commercial;
 KW therapeutic; industrial; fermenting; sugar source; metabolite; vaccine;
 KW biochip technology; antibacterial; modulator of nucleic acid expression;
 KW contig; ds.
 XX Enterococcus faecalis.
 OS
 XX
 XX US2002120116-A1.
 PN
 XX
 XX 29-AUG-2002.
 PD
 XX
 XX 04-MAY-1998; 98US-00070927.
 PF
 XX
 XX 04-MAY-1998; 98US-00070927.
 PR
 XX
 XX (KUNSCH C A.
 PA (DILLON P J.
 PA (BARA/) BARASH S.
 XX
 XX Kunsch CA, Dillon PJ, Barash S;
 PI
 XX
 XX WPI; 2002-750065/81.
 XX
 XX Computer readable medium having recorded on it a Enterococcus faecalis
 PT nucleotide sequence useful for detecting diseases related to Enterococcus
 PT infections in animals.
 PT
 XX
 XX Claim 1; Page; 119pp; English.
 PS
 XX
 XX The present invention relates to a new computer readable medium with an
 CC Enterococcus faecalis nucleotide sequence. The invention is useful to
 CC diagnose the presence of E.faecalis in a sample or determining the
 CC presence of a specific microbe in a sample. The invention is also useful
 CC for modulating the growth or pathogenicity of E.faecalis, in a vaccine to
 CC confer resistance to Enterococcal infection, for commercial, therapeutic
 CC and industrial purposes, and for fermenting a particular sugar source or
 CC to produce a particular metabolite. The invention is useful for detecting
 CC diseases related to Enterococcus infections in animals, and for detecting
 CC E.faecalis using biochip technology. The present nucleic acid sequence
 CC represents an Enterococcus faecalis contig DNA sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at <http://seqdata.uspto.gov>
 XX
 XX Sequence 5277 BP; 1699 A; 946 C; 911 G; 1705 T; 0 U; 16 Other;
 SQ
 Query Match 99.9%; Score 1432.8; DB 6; Length 5277;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1431; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAAGAGTAATATGGTTAGACGTGATTTACGATTACAGGATTAATAGCATTTAGCA 60
 DB 1046 ATGAAAGAGTAATATGGTTAGACGTGATTTACGATTACAGGATTAATAGCATTTAGCA 1105
 QY 61 CACGCGTTACAAAATTTCTGCAGCTGATGAATGATTTATTTATTTCCAAATGAATCCTCAA 120
 DB 1106 CACGCGTTACAAAATTTCTGCAGCTGATGAATGATTTATTTATTTCCAAATGAATCCTCAA 1165
 QY 121 CAATTTATTTCAAGAAAGTGTATCATAGCGCTTTTTCGACGCTTAGCCTCGTTTCAA 180
 DB 1166 CAATTTATTTCAAGAAAGTGTATCATAGCGCTTTTTCGACGCTTAGCCTCGTTTCAA 1225
 QY 181 GAACGAATTCGATCAAGAGGCACATTTACAATCATGTGCGGCAACCATTTAGATTTATTT 240
 DB 1226 GAACGAATTCGATCAAGAGGCACATTTACAATCATGTGCGGCAACCATTTAGATTTATTT 1285
 QY 241 TCACGTTTGAACGCAAAATTTACCGATTGCGAGGCAATTTATTTATGAAGATATCTTGT 300
 DB 1286 TCACGTTTGAACGCAAAATTTACCGATTGCGAGGCAATTTATTTATGAAGATATCTTGT 1345
 QY 301 GGCTTTGGGCAAGCGGGACCGAGCTATCGCTTTTTCGACGAAATATATATTCAG 360
 DB

Db 1346 GGCTTTGGGCAAGCGGGACCGAAGCTATGCGCTTTTGTGAAGAAAAATAATTTTCAG 1405
 QY 361 TCCTTTCTCTTTTCAAGATGCCCTATTTGATCGCTCTGAAGAAATTAAGAAAGAAAGATGGC 420
 DB 1406 TCCTTTCTCTTTTCAAGATGCCCTATTTGATCGCTCTGAAGAAATTAAGAAAGAAAGATGGC 1465
 QY 421 AGCAAGTACCAAGTGTTTTACGCCCTATTTACAATAAATGGAAGAGGGCCCTAAAGAAACA 480
 DB 1466 AGCAAGTACCAAGTGTTTTACGCCCTATTTACAATAAATGGAAGAGGGCCCTAAAGAAACA 1525
 QY 481 CCGATTCTCTGTTTCTATACAGCTGAAATAATTTTGTAGTGGTCTCTTTTCCAGAAAGAG 540
 DB 1526 CCGATTCTCTGTTTCTATACAGCTGAAATAATTTTGTAGTGGTCTCTTTTCCAGAAAGAG 1585
 QY 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACACTATAGTGTGCGGAA 600
 DB 1586 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACACTATAGTGTGCGGAA 1645
 QY 601 GAAACAGCCAGAGGGCGCTTAAATACCTTTTATTTGATCAAAAACTTCAATCTATGAAAT 660
 DB 1646 GAAACAGCCAGAGGGCGCTTAAATACCTTTTATTTGATCAAAAACTTCAATCTATGAAAT 1705
 QY 661 AAGCGTGAATTTCTTATCAGGATCAAAACGAGTCACTGCTCTCTTTTAAAGAACGGGA 720
 DB 1706 AAGCGTGAATTTCTTATCAGGATCAAAACGAGTCACTGCTCTCTTTTAAAGAACGGGA 1765
 QY 721 GAACTTTGATTTGCGACCATTTGGCAAGAGCTTGCATCTGTGCTCTCTAGCTTAAGTAAA 780
 DB 1766 GAACTTTGATTTGCGACCATTTGGCAAGAGCTTGCATCTGTGCTCTCTAGCTTAAGTAAA 1825
 QY 781 GAAACCTTTCAAAAAAGAAATTAGCTTTGGCGGACCTTTTACAATATGATCTATAGTGCCTT 840
 DB 1826 GAAACCTTTCAAAAAAGAAATTAGCTTTGGCGGACCTTTTACAATATGATCTATAGTGCCTT 1885
 QY 841 CCACACAAAAAGAGGAGAGCTTATTTCAAGAAAAATTTTCGTTATTTCAATGACAAATGAC 900
 DB 1886 CCACACAAAAAGAGGAGAGCTTATTTCAAGAAAAATTTTCGTTATTTCAATGACAAATGAC 1945
 QY 901 CCAGAAATGTTTGTTCAGTGCACAAAGGGGAGAGGGGTACCTTATATTTGATGCCGCA 960
 DB 1946 CCAGAAATGTTTGTTCAGTGCACAAAGGGGAGAGGGGTACCTTATATTTGATGCCGCA 2005
 QY 961 ATGCGACAACTGAATCAAACTGGTTGGATGCACAACTCGCTTTAAGAAATGATTTACTGCTCT 1020
 DB 2006 ATGCGACAACTGAATCAAACTGGTTGGATGCACAACTCGCTTTAAGAAATGATTTACTGCTCT 2065
 QY 1021 TTTTGTAGTTAAAAATTTTACACATCGATTGGCGTGGGTGGAATAATCTTTCAAAAAATG 1080
 DB 2066 TTTTGTAGTTAAAAATTTTACACATCGATTGGCGTGGGTGGAATAATCTTTCAAAAAATG 2125
 QY 1081 TTGATTGATGATGCTGCCAATAATATCGTGGCTGGCAATGGCTGGCTTCAACAGGA 1140
 DB 2126 TTGATTGATGATGCTGCCAATAATATCGTGGCTGGCAATGGCTGGCTTCAACAGGA 2185
 QY 1141 ACGGACGCTGCTCTTATTTTCGATTTTAAATCCAATTTATCCAATTTCCAGTCAAAAAATTTGAT 1200
 DB 2186 ACGGACGCTGCTCTTATTTTCGATTTTAAATCCAATTTATCCAATTTCCAGTCAAAAAATTTGAT 2245
 QY 1201 AATGACGCCAGTTCATCAAAAAATATCTTCCAGAACTTAAAGCAAGTGCACAAAGTAT 1260
 DB 2246 AATGACGCCAGTTCATCAAAAAATATCTTCCAGAACTTAAAGCAAGTGCACAAAGTAT 2305
 QY 1261 ATTGATCAACCAATCTAATGAACGAGCTTTACAAAGCAATATCATGTACATTTAGGA 1320
 DB 2306 ATTGATCAACCAATCTAATGAACGAGCTTTACAAAGCAATATCATGTACATTTAGGA 2365
 QY 1321 GAAATTTATCAAAAAACCATTTGTGATTTATGATCAAGTAAAAAACAACATTTGTTCTA 1380
 DB 2366 GAAATTTATCAAAAAACCATTTGTGATTTATGATCAAGTAAAAAACAACATTTGTTCTA 2425
 QY 1381 TATGAAGCGAGCAAGAAATTTATCAAGAAATGAACAAATCCAGGTTTCAATAA 1434
 DB 2426 TAKSAAGCGAGCAAGAAATTTATCAAGAAATGAACAAATCCAGGTTTCAATAA 2479

RESULT 5

```
ADH83427
ID ADH83427 standard; DNA; 966 BP.
XX
AC ADH83427;
XX
DT 22-APR-2004 (first entry)
XX
DE Enterococcus faecalis polynucleotide #1312.
XX
KW Enterococcus faecalis infection; transcription regulatory element;
KW antibacterial; gene; ds.
XX
OS Enterococcus faecalis.
XX
PN US6617156-B1.
XX
PD 09-SEP-2003.
XX
PF 13-AUG-1998; 98US-00134000.
XX
PR 15-AUG-1997; 97US-0055778P.
XX
PA (DOUC/) DOUCETTE-STAMM L A.
XX (BUSH/) BUSH D.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI, 2003-895394/82.
DR P-PSDB; ADH86832.
XX
PT New nucleic acid comprising a sequence encoding an Enterococcus faecalis
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating E. faecalis infection.
XX
PS Disclosure; SEQ ID NO 1312; 193pp; English.
XX
CC The invention relates to Enterococcus faecalis polynucleotides and
CC polypeptides. The invention also relates to a recombinant expression
CC vector comprising a polynucleotide operably linked to a transcription
CC regulatory element, a cell comprising a recombinant vector, a method for
CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising
CC a sequence not given in the specification, a recombinant vector
CC comprising the nucleic acid and a cell comprising the recombinant vector.
CC The polynucleotides can be used to detect the presence of E. faecalis in
CC a sample. The sequences are useful for preparing a composition for
CC diagnosing or treating Enterococcus faecalis infection. This sequence
CC represents an E. faecalis polynucleotide of the invention.
XX
SQ Sequence 966 BP; 325 A; 172 C; 191 G; 278 T; 0 U; 0 Other;
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Query Match 65.7%; Score 942; DB 10; Length 966;
Best Local Similarity 99.9%; Pred. No. 5.7e-226;
Matches 953; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY 1 ATGAAAAGAGTAATATGCTTTAGACGCTGATTTACGATTACAGGATAATAAGCATTAGCA 60
DB 13 ATGAAAAGAGTAATATGCTTTAGACGCTGATTTACGATTACAGGATAATAAGCATTAGCA 72
QY 61 CACGGTTTACAAAATCTGACGCTGATGAATGATTTATTTCCAAATGAATCCTCAA 120
DB 73 CACGGTTTACAAAATCTGACGCTGATGAATGATTTATTTATTTCCAAATGAATCCTCAA 132
QY 121 CAATTTATTCAAGAAAGTGCTAATCATAACTGCTTTTTCGAAAGCTTAGCCTCGTTCAAA 180
DB 133 CAATTTATTCAAGAAAGTGCTAATCATAACTGCTTTTTCGAAAGCTTAGCCTCGTTCAAA 192
QY 181 GAACGAATCGATCAAGAGGCAATTTACAAATCATGGTCGGCGAACCAATTAGATTTATTT 240
DB 193 GAAAGCAATCGATCAAGAGGCAATTTACAAATCATGGTCGGCGAACCAATTAGATTTATTT 252
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RESULT 6

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ADH83428
ID ADH83428 standard; DNA; 609 BP.
XX
AC ADH83428;
XX
DT 22-APR-2004 (first entry)
XX
DE Enterococcus faecalis polynucleotide #1313.
XX
KW Enterococcus faecalis infection; transcription regulatory element;
KW antibacterial; gene; ds.
XX
OS Enterococcus faecalis.
XX
PN US6617156-B1.
XX
PD 09-SEP-2003.
XX
PF 13-AUG-1998; 98US-00134000.
XX
PR 15-AUG-1997; 97US-0055778P.
XX
PA (DOUC/) DOUCETTE-STAMM L A.
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PA (BUSH/) BUSH D.
XX Doucette-Stamm LA, Bush D;
XX WPI; 2003-895394/82.
DR P-PSDB; ADH86833.
XX
XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating E. faecalis infection.
XX
XX Disclosure; SEQ ID NO 1313; 193pp; English.
XX
XX The invention relates to Enterococcus faecalis polynucleotides and
CC polypeptides. The invention also relates to a recombinant expression
CC vector comprising a polynucleotide operably linked to a transcription
CC regulatory element, a cell comprising a recombinant vector, a method for
CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising
CC a sequence not given in the specification, a recombinant vector
CC comprising the nucleic acid and a cell comprising the recombinant vector.
CC The polynucleotides can be used to detect the presence of E. faecalis in
CC a sample. The sequences are useful for preparing a composition for
CC diagnosing or treating Enterococcus faecalis infection. This sequence
CC represents an E. faecalis polynucleotide of the invention.
XX
XX Sequence 609 BP; 225 A; 109 C; 111 G; 164 T; 0 U; 0 Other;
SQ

Query Match 41.6%; Score 597; DB 10; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.7e-139;
Matches 608; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 827 TCTATAGTCGGTTTCACACAAAAGAGGAGCTATTCAAGAAAATTCGTTATATTC 886
DB 1 TCTATAGTCGGTTTCACACAAAAGAGGAGCTATTCAAGAAAATTCGTTATATTC 60
QY 887 AATGACAAATCACCAGAAATGTTGTCAAGTGGCAAAAAGGGAGAC-GGGGTACCCCT 945
DB 61 AATGACAAATCACCAGAAATGTTGTCAAGTGGCAAAAAGGGAGACGGGGTACCCCT 120
QY 946 ATAATTGATCGCGCAATCGCACAACTGAATCAAACTGGTGGATGCACAATCGTTAAGA 1005
DB 121 ATAATTGATCGCGCAATCGCACAACTGAATCAAACTGGTGGATGCACAATCGTTAAGA 180
QY 1006 ATGATTACGCTCTTTTATTAGTAAATTTACACATCGATGCGGTGGGTCAAAA 1065
DB 181 ATGATTACGCTCTTTTATTAGTAAATTTACACATCGATGCGGTGGGTCAAAA 240
QY 1066 TACTTTCAAAAATGTTGATTGACATGATGCTGCCAATAATCGGTGGTGGCAATGG 1125
DB 241 TACTTTCAAAAATGTTGATTGACATGATGCTGCCAATAATCGGTGGTGGCAATGG 300
QY 1126 GCTGCTTCAACAGGAACGACGCTGTCCCTTATTTTCGGATTTTAAATCCAAATTCAG 1185
DB 301 GCTGCTTCAACAGGAACGACGCTGTCCCTTATTTTCGGATTTTAAATCCAAATTCAG 360
QY 1186 TCAAAAATTTGATAATGACGGCAGTTTCATCAAAAATATGTTCCAGAACTTAAGCA 1245
DB 361 TCAAAAATTTGATAATGACGGCAGTTTCATCAAAAATATGTTCCAGAACTTAAGCA 420
QY 1246 GTGCCACAAAGTATATTCATCAACCAATCTAATGAACGAAGCCCTTACAAACGCAATAT 1305
DB 421 GTGCCACAAAGTATATTCATCAACCAATCTAATGAACGAAGCCCTTACAAACGCAATAT 480
QY 1306 CATGTACATTTAGGAGAAAATATCCAAACCCATTTGCGATTTATGTCATCAAGTAAAAA 1365
DB 481 CATGTACATTTAGGAGAAAATATCCAAACCCATTTGCGATTTATGTCATCAAGTAAAAA 540
QY 1366 CAACATTTGTTCTATATGAGCGAGCAAGAAATTCATCAGAAATGAACATTCAGG 1425
DB 541 CAACATTTGTTCTATATGAGCGAGCAAGAAATTCATCAGAAATGAACATTCAGG 600
QY 1426 TTTCATAA 1434
|||||

DB 601 TTTCATAA 609

RESULT 7
ABQ70791
ID ABQ70791 standard; DNA; 2460 BP.
XX
XX ABQ70791;
AC
XX 29-AUG-2003 (revised)
DT 29-AUG-2002 (first entry)
XX
XX Listeria monocytogenes 4b contig DNA sequence #733.
DE
XX Antibacterial; Listeria; food contamination; mutational analysis;
KW infection; ds.
XX
XX Listeria monocytogenes ATCC 19115.
OS
XX WO200228891-A2.
PN
XX 11-APR-2002.
PD
XX 04-OCT-2001; 2001WO-FR003061.
PF
XX 04-OCT-2000; 2000FR-00012697.
PR
XX (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA
PI Kunst F, Glaser P;
XX
XX WPI; 2002-332479/37.
DR
XX New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators.
XX
XX Claim 14; SEQ ID NO 3604; 180pp; French.
PS
XX The present invention relates to nucleic acid sequences (ABQ67188-
CC ABQ71212) from Listeria sp. The sequences are useful as probes and
CC primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of gene
CC expression. Proteins encoded by the nucleic acid sequences can be used to
CC screen for compounds that modulate gene expression, replication and
CC pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in anti-
CC Listeria vaccines. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated
CC on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 2460 BP; 774 A; 410 C; 564 G; 712 T; 0 U; 0 Other;

Query Match 36.7%; Score 526.4; DB 6; Length 2460;
Best Local Similarity 61.6%; Pred No. 1.4e-121;
Matches 883; Conservative 0; Mismatches 536; Indels 15; Gaps 2;

QY 1 ATGAAAAGAGTAATATGCTTTAGAGCGTATTTACGATTACAGGATAATAAGCATTAGCA 60
DB 241 ATGACTTCGGTAAATGCTGTTTCGGAGAGATCTTCGAGTAAACGATAATAAGCTCTCTAT 300
QY 61 CACGGTTACAAAATTCGACGCTGATGAATGATTTTATTATTCGAATGAATCCTCAA 120
DB 301 CATGC-----TTGTAAGAGAGACGATTTGCTTTTGTATTATTCGAAGTAATCCAGCA 351
QY 121 CAATTTATCAAGAAAGTCTAATCATAAACGCTTTTTCGAAGCTTAGCCTCGTTCAAA 180
DB 352 CAGTTTCATCAGGAAGTCCTAGCCACCAAGCTTTTTCGAAGTGTGCTCATTTTAAG 411
QY 181 GAACGAATCGATCAAGAGGCACATTTACAAATCATGTCGGCGAACCATTAGATTTATT 240
|||||

Db 412 CAAGAAATCGATAAAACCTGGCGCATTTTACAAATCATGTTGGTGAAACCGATAGAATGCTTC 471
Qy 241 TCAGGTTGAAACCCAAATTTACCCGATTTGGCAGCCATTTATTTTAATGAAGTACTTGT 300
Db 472 CAACAACCTTAAAGATTCGCTACCAAGCTGGGATAAAGTTTATTTTCAACCGTGATGAACA 531
Qy 301 GGCTTTGGGGCAAGCGGACACGCAAGCTATGCGCTTTTGTGAAGAAAAATAATTTTCAG 360
Db 532 GGATACGGAGCAAGCGGATGAGCGCGCAAGCGTCTTTTGACGAAACAAAATCGAG 591
Qy 361 TCTTTCTCTTTCAAGATGCTATTTTGCATGGCTCTCGAAGAAATTAAGAAGACGATGGC 420
Db 592 GTTCAAGCTTCCACGATAGCTATCTCTCAITTCAGCGGAAGAAAGTAAGAAATCTCCAAACA 651
Qy 421 AGCAAGTACCAAGTGTTTACGCCCTATTTACAAATAATGGAAGAGCGCCTAAAGAAACA 480
Db 652 GAATFACTATAAAATTTTACCCCTTATTTATAAAAAATGGCGGAAAGAAATAAAGAAACG 711
Qy 481 CCGATTCTGTTTCTCTATACAGCTGAAAAAATTTTATAGTGGTGTCTTTTTTCCAGAAAGAG 540
Db 712 CCGTTCAAAGTGACTTTTAAGCATGAGNATATCCGGAAGAAAGCTTGTCTCTGAATAT 771
Qy 541 GAAGCAGCTTATCGTGACAGATTCGAGGATTCCTTTTAAACACATATAGTGTGGCGAA 600
Db 772 GAAGAACAAATTTGCGGAAATGACT-----AGCGATTTACCGATTTAGATATTTGGTGAA 825
Qy 601 GAAACAGCGAAGCGCTTAATACTTTTATTTGATCAAAAACCTTCAATCCTATGAAAT 660
Db 826 CGAGCAGCGAACACGAGACTTGGCAATTTTATTAACACCATGTGTGACTATGACAAA 885
Qy 661 AAGCGTGATTTCTCTATCAGATCAACAGAGTCATCTGTCTACTTTTAAAGAACGGGA 720
Db 886 GCGAGAGATTTCCCGAACTGGATTAACAAAGCCATTTATACGTTATTTACGACGGGG 945
Qy 721 GAACCTTTGATTCGCACCATTTGGCAAGAGCTTGCAATCTGTGCCCTCTAGCTTAAGTAA 780
Db 946 GAAATCTCGATTCGACGATTTGGCAGACATTTCAAGAAACAGAAAGCAACAGAGGACGA 1005
Qy 781 GAAACCTTCAAAAAGAAATTAGCTTGGCGGACCTTTTACAAATATGATCTATGCGTTT 840
Db 1006 GCTACATTTGAAAAGAACTGTGTAGCGGACCTTTTATAATATGATTTACGTTCTCTTT 1065
Qy 841 CCACAACAAAAGAGGAGCTATTCAAGAAAAATTTTCGTTATATTTCAATGACAAAAATGAC 900
Db 1066 CTTAACCAAAAACAGAGCCGATCAAGAAAAATTTATGTTTTATTTGAATGGAAAAATAC 1125
Qy 901 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGGTACCCCTATATTTGATGCGCGA 960
Db 1126 CGCGAATATTTCAAAGCGTGGCAAGAGGGAAGACTGGTTTCCGCTCGTTGATGCGCG 1185
Qy 961 ATGGCAACCTGAATCAAACTGGTTGGATGCACAATTCGCTTAAAGATGATTTAGCTCTCT 1020
Db 1186 ATGGCCAGTTTGAAGAAACCTGGTTGGATGCAATAATCGACTAAGAAATGATTTACGGCTC 1245
Qy 1021 TTTTATGTTAAAAATTTACACATCGATTTGGGTTGGGTGAAAAATCTTTCAAAAAATG 1080
Db 1246 TTTTAAACAAAGATTTGCTGATTTGATTTGGGTTTGGCGAAAAGTATTTTCAACAATG 1305
Qy 1081 TTGATGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTCTTCAACAGGA 1140
Db 1306 CTGATTTGATTTATGCTCGAGTAAATATTTGTTGGCTGGCAATGGCGCTTCGACTGGA 1365
Qy 1141 ACGGACGCTGCTCTTATTTTCGGATTTTATTTCAATTTATTCGAATTCAGTCAAAAAATTTGAT 1200
Db 1366 ACGGATGCGGTGCCATCTTTAGGATTTTCAACCCCAACGACACAAATCACAAAAATTTGAT 1425
Qy 1201 AATGCGGCCAGTTTCATCAAAAATATGTTCCAGAACTTTAGCAAGTGCCACAAAAGTAT 1260
Db 1426 TCGACTGGGAAATTTATTCGAAAATATGTAAGAGATTTAGCGAATCTACCTGATAAATAT 1485
Qy 1261 ATTCAACCAAAATCTTAATGAACGAGCCCTTACAACAGCAATATCATGTACATTTAGGA 1320
Db 1486 ATTCAACCAAGAAATGTCAGAACTGAGCAGAAAGAGCATGGCTTCTGTAGGA 1545

RESULT 8

AB069245_06
Continuation (7 of 31) of AB069245 from base 600001 (Listeria innocua DNA sequence #684.
WP Sequence split into 31 fragments LOCUS AB069245 Accession Abg69245

WP	Fragment Name	Begin	End
WP	AB069245_00	1	110000
WP	AB069245_01	100001	210000
WP	AB069245_02	200001	310000
WP	AB069245_03	300001	410000
WP	AB069245_04	400001	510000
WP	AB069245_05	500001	610000
WP	AB069245_06	600001	710000
WP	AB069245_07	700001	810000
WP	AB069245_08	800001	910000
WP	AB069245_09	900001	1010000
WP	AB069245_10	1000001	1110000
WP	AB069245_11	1100001	1210000
WP	AB069245_12	1200001	1310000
WP	AB069245_13	1300001	1410000
WP	AB069245_14	1400001	1510000
WP	AB069245_15	1500001	1610000
WP	AB069245_16	1600001	1710000
WP	AB069245_17	1700001	1810000
WP	AB069245_18	1800001	1910000
WP	AB069245_19	1900001	2010000
WP	AB069245_20	2000001	2110000
WP	AB069245_21	2100001	2210000
WP	AB069245_22	2200001	2310000
WP	AB069245_23	2300001	2410000
WP	AB069245_24	2400001	2510000
WP	AB069245_25	2500001	2610000
WP	AB069245_26	2600001	2710000
WP	AB069245_27	2700001	2810000
WP	AB069245_28	2800001	2910000
WP	AB069245_29	2900001	3010000
WP	AB069245_30	3000001	3011208

Query Match 36.2%; Score 518.4; DB 6; Length 110000;
Best Local Similarity 61.2%; Pred. No. 5.1e-119;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

Qy 1 ATGAAAAGAGTAATATGGTTTACGCTGATTTACGATTACAGGATTAAGCAATTAAGCATTAGCA 60
Db 28080 ATGACTTCAGTAATGTGGTTTCGTAGAGATCTTCGAGTAATGATATAAAGCTCTTTAT 28139
Qy 61 CACGCGTTACAAAATCTGCAGCTGATGAATGATTTTATTTATTTCCAAATGAATCCCTCAA 120
Db 28140 CATGCTCTTAAGA-----AGAGATTTAATTTTGTATTTCAGTAAATCCAGAA 28190
Qy 121 CAATTTATTTCAAGAAAGTGCTAATCAACGCTTTTTTTTGCAGCTTAGCTCGTTCAAA 180
Db 28191 CAATTTATCAAGGAAGCCCTAGTCCCAAGCATTTTTTCGAGTGTAGCTCATTTTTCAA 28250
Qy 181 GAACGAATCGATCAAGAGGCAATTTTACAAATCATGTCGGCGCAACCATTAGATTTATTT 240
Db 28251 CAAGAACTAAATAAAAACACCCATTTTGCAAATCATGTTTGGCGAGCCAAATCGAGCTCCTA 28310
Qy 241 TCACGTTTGAACGCAAAATTTACCCGATTTGGCAGGCCATTTATTTTAAATGAAGATACTTGT 300
Db 28311 AAACAATTAAGAAAAAATACCAACTTGGGATAAAGTTTCTTTCACCCGATGAACA 28370
Qy 301 GGCTTTGGGCAAGCGGGACCAAGAGCTATGCGCTTTTTTTTGAAGAAAAATATATTTACG 360

Db 28371 GGCTACGGAGCGAGTCGAGAGCGCTGCCCGAGCATTTCTTTGCTGATAAGGAAATCACA 28430
Qy 361 TCTTCTCTCTTTCAAGATGCGCTATTGTCATGGCTCTGAAGAAATTAAGAAAGACGATGGC 420
Db 28431 GTTCACAGCTATCAGATAGTTACCTTCATTCAGCTGAGAAAGTGAATAATCCGCCACA 28490
Qy 421 AGCAAGTACCAAGTGTGTTTACGCCCTATTACAAATAATGGAAGAGCGCCCTAAAGAAACA 480
Db 28491 GAATACTACAAATCTTCACTCTTACTACAAAAATGGCGGAAGAAATAAAGAAATG 28550
Qy 481 CCGATCTCTGTTCTCTATACAGCTGAAAAAATTTTAGTGGTGTCTTTTCCAGAGAG 540
Db 28551 CCTTTAAAGTCACTTTAAACACGAAAAATTAGGAAAGAAAGCTTATTTCCAAATAT 28610
Qy 541 GNAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAACACATATAGTGTGCGGAA 600
Db 28611 GAGGAACAGTTTAGAGAACTGATTTTTTATGATCAAAAACTTCAATCCTATGAAAT 660
Qy 601 GAAACAGCCAGAAAGCGCTTAAATACTTTTATGATCAAAAACTTCAATCCTATGAAAT 660
Db 28655 AAAGCAGCGAATACAGACTTGCAAACTTTGTAAAGAAAGATTTAGCAGACTATGACAA 28724
Qy 661 AAGCGTGATTTTCTTTATCAGATCAAAACGAGTCACTGTCTACTTTTAAAGAACGGGA 720
Db 28725 GCAAGAGACGTCACGCGCTTGATAAAACGAGTCAATTTATCAGCTATTTACGAAACGGGA 28784
Qy 721 GAACTTTGATTCGCACCATTTGGCAAGCTTGCATCTGTGCCCTTCTAGCTTAAGTAA 780
Db 28785 GAGATTTGATTCGATTCGATTCGAGGACCTTCAAAAAAGAAAGCTTACAGAGGACGA 28844
Qy 781 GAAACCTTTCAAAAAAGAAATAGCTTGGCGGCACTTTTACAAATATGATCTATAGTGCCTTT 840
Db 28845 GCAACATTCGAAAAAGAACTGTGTTGGCGGATTTTATATATGATTTATGTTCTTTT 28904
Qy 841 CCACAAAAAGAGAAAGCTATTCAAGAAAAATTCGTATATTTCAATGACAAAAATGAC 900
Db 28905 CCAGACAAAAAATAGCCTATTCAAGAAAAATATCGTTTATTTGAATGGAAAAATAT 28964
Qy 901 CCAGAAATGTTGTCAGTGGCAAAAGGGGAGCGGGTACCCTATTAATTTGATGCCGA 960
Db 28965 CGCGAAATTTTCAAGAAAGTGGCAAGCGGCAAACTGTTTTTCCGCTTGTGATGCTCG 29024
Qy 961 ATGCAGCAACTGAATCAAACTGGTTGGATGCACAATCGCTTAAGAAATGATTTACTGCTCT 1020
Db 29025 ATGCCCAATTAAGAGACGGGCTGGATGCATAATCGCTGAAGAAATGATCACGCTTCC 29084
Qy 1021 TTTTGTAGTTAAAAATTTACACATCGATTTGGCGTTGGGGTGAAAAATACCTTCAAAAAATG 1080
Db 29085 TTTTAAACGAGGATTTACTAATGATTTGGCGTTTGGCGAAAAATATTTTCAACAAATG 29144
Qy 1081 TTGATGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA 1140
Db 29145 CTAATGATTACGACCCAGCAGTAAATTTGGCGGTTGGCAGTGGCGGCTTCGACTGGA 29204
Qy 1141 ACGGAGCTGCTCCCTTATTTTCGGATTTTATCCAATTTATCCAGTCAAAAAATTTGAT 1200
Db 29205 ACAGATGCAAGTACCGCTATTTTGAATTTTAAATCCAAACCAACCAATCGGAAAAATTTGAT 29264
Qy 1201 AATGACGGCCAGTTCAATCAAAAAATATGTTCCAGAACTTTAAGCAAGTGCACAAAGTAT 1260
Db 29265 CCAGATGGTACATTTATTCGGAATATATGTAAGGAATTTACGGGACTTGCCGGATTAATTC 29324
Qy 1261 ATTCAATCAACCAATCTAATGAACGAGCCTTTACAAACGCAATATCATGTACATTTAGGA 1320
Db 29325 ATTCATCAACGAAAAAATGCTGAAAACAGACGAAAAAGACATGTTGATTTTATGGA 29384
Qy 1321 GAAAAATATCCAAACCCATTTGCGATTTATGATCAAGTAAAAAAACAACATTTGTTCTA 1380
Db 29385 AAAGATTTATCCGCTTCCGATAATTCGACCAATAAGAGCGGCAAAAAATTAGCGATTCGCGGA 29444
Qy 1381 TATGAAGCCGACAAAGAAATTCATCAAGAAATGAACAATCCCAAGGTTTCAATAA 1434
Db 29445 TATGATTTAGCAAGGAGCAATTTCTAGGGGAATATATATGATTAATGATCAATCA 29498

RESULT 9

ABQ67197_05
Continuation (6 of 12) of ABQ67197 from base 500001 (Listeria innocua contig DNA sequence
WP Sequence split into 12 fragments LOCUS ABQ67197 Accession Abq67197

WP	Fragment Name	Begin	End
WP	ABQ67197_00	1	110000
WP	ABQ67197_01	100001	210000
WP	ABQ67197_02	200001	310000
WP	ABQ67197_03	300001	410000
WP	ABQ67197_04	400001	510000
WP	ABQ67197_05	500001	610000
WP	ABQ67197_06	600001	710000
WP	ABQ67197_07	700001	810000
WP	ABQ67197_08	800001	910000
WP	ABQ67197_09	900001	1010000
WP	ABQ67197_10	1000001	1110000
WP	ABQ67197_11	1100001	1163020

Query Match 36.2%; Score 518.4; DB 6; Length 110000;
Best Local Similarity 61.2%; Pred. No. 5.1e-119;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

Qy	1	ATGAAAGAGTAATATGTTTACAGTGATTTAGCATACAGGATTAAGCAATTAAGCAATTAGCA 60
Db	37815	ATGACTTCAGTAATGTGTTTCGTAGAGATCTTCGAGTAAATGATAATAAAGCTCTTTAT 37874
Qy	61	CACGCGTTACAAAATTCGCGAGCTGATGATTTGATTTTATTTCCAAAATGAATCCCTCAA 120
Db	37875	CATGCCCTGTAAGA-----AGAAGATTTAATTTTGTTATTTCAAGTAAATCCAGAA 37925
Qy	121	CAATTTATTCAGAAAAGTGTAAATCATACGCTTTTTTTTGCAGCTTAGCTTCGTTCAA 180
Db	37926	CAATTTATCAAGGAAGCCCTAGTCACCAAGCATTTTTCGGAGTGTAGCTCATTTTCAA 37985
Qy	181	GAACGAATCGATCAAGAGGCACATTTTACAAATCATGTGCGGCGAACCATTTAGATTTATTT 240
Db	37986	CAAGAACTAAATAAAAAACACCCATTTGCAAAATCATGTTTGGCGAGCCAATCGAGCTCCTA 38045
Qy	241	TCAGTTTGAACGCAATTTACCGGATTTGGCAGGCCATTTATTTTAATGAAGATACTTGT 300
Db	38046	AAACAATTTAAAGAAAAAATAACCAACTTGGGATAAAGTTTCTTCAACCGCGATGAACA 38105
Qy	301	GGCTTTGGGCAAGCGGACCCAGCAAGCTATGGCTTTTGTGAAGAAAAATAATTTCCAG 360
Db	38106	GGCTACGAGCGATCGAGAGAGGCTGCCGAGCATCTTTGCTGATAGGAATCACA 38165
Qy	361	TCTTTCTCTTTTCAAGATGCTTATTTGCTATGGCTCTCGAAGAAATTAAGAAACGATGGC 420
Db	38166	GTTCCACAGCTATCACGATAGTTACCTTCATTCAGCTGAAGAAGTGAATAATCCGCCACA 38225
Qy	421	AGCAAGTACCAAGTGTTTAGCCCTTATACAAATTAATGGAAGAGGCGCTTAAAGAACACA 480
Db	38226	GAATACTACAAAATCTTCACTCTTACTACAAAAAATGGCGGAGAAATAAAGAAATG 38285
Qy	481	CCGATTCCTGTTCTTATACAGCTGAAAAAATTTTATGTCGTCTTTTCCAGAAAGAG 540
Db	38286	CTTTAAAGTCACTTTTAAACCCAGAAAAAATTAGGAAGAAAGCTTATTTCCAAATAT 38345
Qy	541	GAACGAGCTTATCGTGAACAGATTTGCGAGGATTCCTTTTAAACACATATAGTGTGCGGAA 600
Db	38346	GAGAAACAGTTTAGAGAACTGATTT-----CAAGATTTACCAGCTTTGATTTCCGCTGAA 38399
Qy	601	GAACAGCGAAGCGCGCTTAAATACCTTTTATGATCAAAAACTTCAATCCTATGAAAT 660
Db	38400	AAAGCAGCAATACGAGACTTGCAAACTTTGTAAGAAGAAAGTTTAGCAGACTATGACAAA 38459
Qy	661	AAGCGTATTTTCTTATCAGGATCAACGAGTCACTGCTACTCTTTTAAAGAACGGGA 720
Db	38460	GCAAGAGACGTCGCCGCGCTTTGATTAACACGAGTCAATTTATCACGCTATTTACGAAACGGGA 38519
Qy	721	GAACTTTTCGATTCGCACCATTTTGGCAAGAGCTTGCATCTGTGCCCTTCTAGCTTAAGTAAA 780

Db	38520	GAGATTTTCGATTCGTACGGTTTGGCAGGCACCTTCAAAAAAGAGAGCTACAGAGACGA	38579
Qy	781	GAACCTTTCAAAAAAGAAATAGCTTGGCGGCACTTTTACAAATATGATCTATAGTGGCTTT	840
Db	38580	GCAACATTCGAAAAAGAACTGTGTGGCGCATTTTATAATATGATTTATGTTCTCTTT	38639
Qy	841	CCACAAACAAAAGAGGAAGCTATTCAAGAAAAATTTTCGTTATATTCAATGACAAATGAC	900
Db	38640	CCAAAGCAAAAAATGAGCCTATTCAAGAAAAATTTATCGTTTTATTGAATGGGAAAAATAT	38699
Qy	901	CCAGAAATGTTTTCAGTGCACAAAAGGGAGACGGGTACCCCTATAATTTGATGCGCA	960
Db	38700	CGCGAATTTTCAAGAAGTGCACAGCGGCAAACTCGTTTTCCGTTGTCGATGCTGGC	38759
Qy	961	ATGCGACAACATGAATCAAACTGGTTGGATGCACAAATCGCTTAAAGAATGATTACTGCGCTCT	1020
Db	38760	ATGCGCCAAATTAAGAGACGGGTGGATGATTAATCGGCTAAGAAATGATCACGGCTTCC	38819
Qy	1021	TTTTTAGTTAAAAATTTACATCGATTTGGGTTGGGGTGAAAAATACCTTTCAAAAAATG	1080
Db	38820	TTTTTTAACGAGAGATTTACTAAATTTGATTTGGCGTTTTCGCGAAAAATATTTTCAACAAATG	38879
Qy	1081	TTGATTCGACTATGATGCTGCCAAATAATATCGTGGCTGGCAATGGGCTGCTTCAACAGGA	1140
Db	38880	CTAATTTGATTACGACCCAGCGAGTAATATTGGCGGTTGGCAGATGGGCGGCTTCGACTGGA	38939
Qy	1141	ACGGACGCTGCTCCCTTATTTTCGGATTTTAAATCCAATTTATCCAGTCAAAAAATTTTAT	1200
Db	38940	ACAGATCGAGTACCGTATTTTAGAATTTTAAATCCAACACCCCAATCGGAAAAATTTGAT	38999
Qy	1201	AATGACGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCCACAAAAGTAT	1260
Db	39000	CCAGATGGTACATTTATTTCGGAATATGTAAGGAATTTACGGGACTTTGCGGATAAATTC	39059
Qy	1261	ATTCATCAACCAATCTAATGAACGAAGCCCTTACAAAGCAATATCATGTACATTTTAGGA	1320
Db	39060	ATTCATCAACAGAAAAAATCTGTAACAGACAGACGAGCAAGAAATTTAGCGATTGCGCGA	39179
Qy	1321	GAATAATTATCAAAACCCATTGTCGATTTATGCATCAAGTAAAAAACAACCAATTTGTTCTA	1380
Db	39120	AAAGATTATCCGTTCCGATAATCGACATAAAGAGCGAGCAAAATTTAGCGATTGCGCGA	39179
Qy	1381	TATGAGCGGCAAGAAATTCATCAAGAAATGAACAAATCCAGGTTTCAATAA	1434
Db	39180	TATGAGTTTATGCAAGGAGCATTTCTAGGGGAATATATAGATAATGAATCAATCA	39233

RESULT 10

ABAO3041_06

Continuation (7 of 30) of ABAO3041 from base 600001 (Listeria monocytogenes EGD-e genome

WP Sequence split into 30 fragments LOCUS ABAO3041 Accession ABAO3041

WP	Fragment Name	Begin	End
WP	ABAO3041_00	1	110000
WP	ABAO3041_01	100001	210000
WP	ABAO3041_02	200001	310000
WP	ABAO3041_03	300001	410000
WP	ABAO3041_04	400001	510000
WP	ABAO3041_05	500001	610000
WP	ABAO3041_06	600001	710000
WP	ABAO3041_07	700001	810000
WP	ABAO3041_08	800001	910000
WP	ABAO3041_09	900001	1010000
WP	ABAO3041_10	1000001	1110000
WP	ABAO3041_11	1100001	1210000
WP	ABAO3041_12	1200001	1310000
WP	ABAO3041_13	1300001	1410000
WP	ABAO3041_14	1400001	1510000
WP	ABAO3041_15	1500001	1610000
WP	ABAO3041_16	1600001	1710000
WP	ABAO3041_17	1700001	1810000
WP	ABAO3041_18	1800001	1910000
WP	ABAO3041_19	1900001	2010000

WP	ABAO3041_20	2000001	2110000
WP	ABAO3041_21	2100001	2210000
WP	ABAO3041_22	2200001	2310000
WP	ABAO3041_23	2300001	2410000
WP	ABAO3041_24	2400001	2510000
WP	ABAO3041_25	2500001	2610000
WP	ABAO3041_26	2600001	2710000
WP	ABAO3041_27	2700001	2810000
WP	ABAO3041_28	2800001	2910000
WP	ABAO3041_29	2900001	2944528

Query Match

Best Local Similarity

Score 516.8; DB 6; Length 110000;

Best Local Similarity

61.2%; Pred. No. 1.3e-118;

Mismatches 877; Conservative 0; Mismatches 542; Indels 15; Gaps 2;

Qy	1	ATGAAAGAGTAAATATGTTTATAGCTGATTTACAGTATTAACGATTAACAGATTAATAAGCAITAGCA	60
Db	29088	ATGACTTCTGTAATGTGTTTCGGAGAGATCTTCGAGTAAATGATATAAAGCCCTTAT	29147
Qy	61	CACGGTTACAAAATTTCTGCAGCTGATGAATTCATTTATTTATTTCCAAATGAATCTCAA	120
Db	29148	CATGC-----TTGTAAAGAGGACGATTTGCTTTTGTATTTCAAGTAAATCCAGCA	29198
Qy	121	CAATTTATTTCAAGAAAGTGTAAATCATAACGCTTTTTTTTTCGAAGCTTAGCTCGTTCAA	180
Db	29199	CAGTTTCATCACAGGAAGTCTAGCCACCAAGCTTTTTTTTTCGAAGTGTGCTCATTTTAAG	29258
Qy	181	GAACGAATCGATCAAGAGGACATTTACAAATCATGTCGGCGGAACCATTAGATTTATTT	240
Db	29259	CAAGAAGTTGATAAAACCGCGCTTTTACAAATCATGTTTGGTGAACCGGTAGAATCTTA	29318
Qy	241	TCACGTTTGAACCGCAAAATTTACCGATTTCGAGGCCATTTATTTTAAATGAAGTACTTGT	300
Db	29319	AAACAATTTAAAGAAACCGCTACCAAGCTGGGATAAAGTTTATTTCAACCGCGATGAACA	29378
Qy	301	GGCTTTGGGCGCAAGGGCGGACCAAGCTATGCGCTTTTTTTTGAAGAAAAATATATTTTCAG	360
Db	29379	GGTTACGGAGCAGAGCGGAGCGAAGCGGCGAAAACTTTCTTTGACGAACAAGAAATAGAG	29438
Qy	361	TCCTTCTCTTTTCAAGATGCTTATTTGTCATGGCTCTGAAAGAAATTAAGAAAGCAATGGC	420
Db	29439	GTTTCAAGCCTTCCACGACAGCTACCTTCACTCAGCAGAAAGAGTAAAAAATCCCCACA	29498
Qy	421	AGCAAGTACCAAGTGTTTACGCCCTTATTACATTAATGGAAGAGGCGCTTAAAGAAACA	480
Db	29499	GAATACTACAAAATCTTTTATCCCTTACTATAAAAAATGGCGTGAAGAAATTAAGAAACG	29558
Qy	481	CCGATTTCTGTTTCTCTATACAGCTGAAAAAATTTTTTAGTGGCTGTCTTTTCCAGAAAG	540
Db	29559	CCGTTCAAAGTGACTTTTAAAGGCAGATAATATACGAAGAAAGAAACTTATTTCCAAAAATC	29618
Qy	541	GAAGCAGCTTATCGTGAACAGATTCGAGGATTCCTTTTAAACACACTATAGTGTGGCGAA	600
Db	29619	GAAGAACAGTTCGCCGAATATGACTTCGGATTTGCCGATATTTAGATTTCT-----GGTGA	29672
Qy	601	GAACAGCCAGAGGCGCTTTAATACTTTTATGATCAAAAACCTTCAATCTCTATGAAAT	660
Db	29673	AAAAACAGCAACACAAGACTTCGCGAATTTTATTAACACGATGTGCTGACTATGACAAA	29732
Qy	661	AAGCGTGATTTTCTCTTATCAGGATCAAAACGAGTCATCTGTCTACTTTTTTAAAGAACGGGA	720
Db	29733	CGAGAGATTTTCCAGAACTGGNATAAAGAGCCATTTATCGCTATTTACGACAGGA	29792
Qy	721	GAACTTTTCGATTCGCACCATTTTGGCAAGAGCTTGCATCTGTGCTTCTAGCTTTAAGTAA	780
Db	29793	GAAATCTCGGTTCCGACGATTTTGGCAGGCATTTCAAGAAAAACGAAGCTACAGAAGACGA	29852
Qy	781	GAACCTTCAAAAAGAAATTAGCTTTCGGCGCACTTTTACAAATATGATCTATAGTGGTTT	840
Db	29853	GCCATATTGAAAAAGAGCTTTGTTGGCGTGACTTTTATATAATATGATTTATGTTCTTTT	29912
Qy	841	CCACAAACAAAAGAGGAAGCTATTTCAGAAAAAATTTTCGTTATATTCAATGACCAAAATGAC	900

Db 29913 CCTAACCAAAAAGAGCGCTATCAAGAAAAATTATCGTTTTTGAATGGAAAAACAAC 29972

Qy 901 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGAGAGCGGCTACCCCTATTAATTTGATGCCGCA 960

Db 29973 CGCGAAATTTTCAAGAGCATGGCAAGAGGGAAGACTGGTTTTTCCGCTCGTTGATGCGACG 30032

Qy 961 ATGGCACAACGAATCAAACTGGTTGGATGACAAATCGCTTAAAGAAATGATTACTGCTCT 1020

Db 30033 ATGCCCCAGCTGAAAGAACTGGTTGGATGCAATATCAATTAAGATGGTTACGGCTCC 30092

Qy 1021 TTTTGTAGTTAAAAATTACACATCGAATGGCGTTGGGTGGAATAATCTTCAAAAAATG 1080

Db 30093 TTTTAAACGAAGACTTGTGATTCGATTTGGCGAATTTGGGGAATAATTTTCAACAATG 30152

Qy 1081 TTGATTGACTATGCTGCCAATATATCGTGGCTGGCAATGGCTGCTTCAACAGGA 1140

Db 30153 CTGATTGATTATGATCTCGAGTAATATTTGGTGGCTGGCAATGGGCGCTTCGACTGGA 30212

Qy 1141 ACGGACGCTGCCCTTATTTTCGGATTTTAAATCCAATTTATCCAGTCAAAAAAATTTGAT 1200

Db 30213 ACAGATCGGTCGCATCTTTAGGATTTTCAACCCACGACACAATCACAAAATTTGAT 30272

Qy 1201 AATGACGCGCAGTTTCATCAAAAAATATGTTCCAGAACTTAAAGCAAGTCCCAAAAGTAT 1260

Db 30273 CCGACGGGAATTTTATTCGAAATATGTAAGAGAGTTAGCGAATTTACCTGATAAATTC 30332

Qy 1261 ATTCAATCAACCAAAATCTAATGAACGAAGCTTTTCAACGCAATATCATGTACATTTAGGA 1320

Db 30333 ATTCATCAACCAAGAAAAATGTCAGAAATAGAGCAGAAAGAGTATGGTTTGTCTATTAGGA 30392

Qy 1321 GAAATATATCAAAACCCATTTGCTGATTTGCTGATTCATCAAGTAAAGAAACAACATTTGTTCTA 1380

Db 30393 AAAGACTATCCATTCCTTTAATGACCAATAAGAACGCGTAAATTTAGCCATTCGACGC 30452

Qy 1381 TATGAAGCAGCAAGAAATTCATCAAGAAATGAACAATCCAAAGTTTCAATAA 1434

Db 30453 TAGAGTTTAGCAAGAGCATTTAGGGGAATATATAGACAATGAGTCAATCA 30506

RESULT 11

ID ABQ68877 standard; DNA; 1451 BP.

XX AC ABQ68877;

XX AC

XX 29-AUG-2003 (revised)

DT 29-AUG-2002 (first entry)

XX DE Listeria monocytogenes 4b contig DNA sequence #1643.

XX Antibacterial; Listeria; food contamination; mutational analysis;

KW infection; ds.

XX Listeria monocytogenes ATCC 19115.

OS

XX WO200228891-A2.

PN 11-APR-2002.

XX 04-OCT-2001; 2001WO-FR003061.

XX 04-OCT-2000; 2000FR-00012697.

XX (INSP) INST PASTEUR.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Kunst F, Glaser P;

XX WPI; 2002-332479/37.

XX New genomic sequences from Listeria species, useful for detection,

PT treatment and prevention of infection, also related polypeptides,

PT antibodies and modulators.

XX Claim 14; SEQ ID NO 1690; 180pp; French.

PS

XX The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)

XX

SQ Sequence 1451 BP; 443 A; 308 C; 327 G; 373 T; 0 U; 0 Other;

Query Match 29.1%; Score 416.8; DB 6; Length 1451;

Best Local Similarity 59.0%; Pred. No. 3.7e-94;

Matches 759; Conservative 0; Mismatches 512; Indels 15; Gaps 2;

Qy 1 ATGAAAAGACTAATATGTTTACGCTGATTACGATTACAGGATAATAAGCATTAGCA 60

Db 39 ATGACTTCGGTAATGTGTTTCGGAGAGATCTTCGAGTAACGATAATAAGCTCTCTAT 98

Qy 61 CACGCGTTACAAAATCTGCAGCTGATGAATTTGATTTTATTTCCAAATGAATCTCAA 120

Db 99 CATGC-----TTGTAAGAGGAGCATTTGCTTTGTTTATTTCAAGTAATCCAGCA 149

Qy 121 CAATTTATTCAGAAAGTGCTAATCATACGCTTTTTTTTGCAGCTTAGCCTCTTCAA 180

Db 150 CAGTTTCATCAGGAAGTCTCTAGCCACCAAGCTTTTTTTGCAAGTGGCTCATTTAAG 209

Qy 181 GAACGAATCGATCAAGAGGCACATTTACAAATCATGTCGCGCAACCATTAGATTTATT 240

Db 210 CAAGAAATCGATAAAACCTGCGCATTTTACAAATCATGTTTGGTGAACCATAGATGCTT 269

Qy 241 TCAGTTTGAACGCAAAATTACCGGATTGGCAGGCCATTTATTTTAAATGAAGATACTTGT 300

Db 270 CAACAATTAAGATTTCGCTACCAAGCTGGGATAAAGTTTATTTCAACCGTGAAGAA 329

Qy 301 GGCTTTGGGCAAAAGCGGACCAAGCAAGCTATGCGCTTTTTTGAAGAAATAATATTTCAG 360

Db 330 GGATACGAGCAAAAGCGGATGAGCGCGCAAGCTTCTTTGACGAACAAAAAATTCGAG 389

Qy 361 TCTTTCTCTTTTCAAGATGCTATTTGCATGGCTCTGAAGAAATTTAGAAAGACGATGGC 420

Db 390 GTTCAAGCTTTCCACGATAGCTATCTTCAATTCACGCGGAAGAAAGTAAAGAAATCTT 449

Qy 421 AGCAAGTACCAAGTGTTTTACGCCCTTATTAATAATGAAGAGAGCGCTTAAAGAAACA 480

Db 450 GAATACTATAAATTTTTTACCCCTTATTAATAAATGGCGCGAAGAAATAAAGAAACG 509

Qy 481 CCGATTCTCTGTTTCTATACAGCTGAAAAAATTTTATAGTCGCTGTCTTTTCCAGAAAG 540

Db 510 CCGTTCAAAGTGACTTTTAAAGCATGAGAAATATCCGGAAGAAAGCTTCTTCTGAAATAT 569

Qy 541 GAAGCAGCTTATCGTGAACAGATTCCGAGGATTCCTTTTAAACACTATAGTCTCGCGCA 600

Db 570 GAAGAAACAATTTGCGGAATGACT-----AGCGATTTTACCGATATTAGATATTGGTGA 623

Qy 601 GAAACAGCCAGAGCGCTTAAATACTTTTATGATCAAAAACTTCAATCTCTATGAAAT 660

Db 624 CGAGCAGCGAACAACGAGACTTTCGGAATTTTATTAACACGATGTTGCTGACTATGACAA 683

Qy 661 AAGCGTGATTTTCTTATCAGGATCAAAACGAGTCTATCTGTCTACTTTTAAAGACGGGA 720

Db 684 GCGAGAGATTTCCCGGAACCTGATAAACAAGCCATTTATCAGCTTATTTTACGAACGGGG 743

Qy 721 GAATCTTCGATTCGACCATTTGGCAAGAGCTTGCATCTGTGCTCTTCTAGCTTAAGTAA 780

Db 744 GAAATCTCGATTTCGACGATTTGGCAGACACTTCAAGAAACAGAAAGCAAGAGACGA 803


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QY 669 TTTTCCTTATCAGGATCAAGAGTCATCTGTCTACTTTTTTAAGAACGGAGAACTTTC 728
Db 696 TTTTCCAGCGCAGTAGGACGAGTCGGTGTCTCTCTTTTTTAAGATAGAGCTATTGG 755
QY 729 GATTCCGACCATTTGGCAAGAGCTTGCATCTGTGCTTCTAGCTTAAAGTAAAGAACTT 788
Db 756 CATTCGACGGTATATCACGCTGTGCGTCAAGCACAAATAGCTAGGGCAAGCTACTTT 815
QY 789 CAAAAAGAAATAGCTTGGCGGAGCTTTTACATATGATCTATAGTGGTTCACACACA 848
Db 816 TTTTAAAGAAATAGCTTGGAGAGACTTTTACAATATGCTATGCTATGCTTATCTCTGATCA 875
QY 849 AAAAGAGAGACTTTCAGAAABATTCGTTTATATCAATGGAACAAATGACCCAGAAAT 908
Db 876 GAAAACTCAGCCTATCCAAAAAGCCCTTTCTCAAAATCGAATGGGTTAATATCTGACTG 935
QY 909 GTTTCGTAAGTGGCAAAAGGGAGACGGGTACCTATATTAATGATGCGCAATGCGACA 968
Db 936 GTTTCAGTTGTGAAGAAGGTAAACGGGTACCTTATGTCGATGCTGCAATGCTTCA 995
QY 969 ACTGAATCAAACTGTGTGATGCAAAATCGCTTAAAGATGATTAAGTCTCTTTTAACT 1028
Db 996 GTTCAAAAGACAGGATGCATAATCGTTTACGAATGATAGTAGCTTCTTTTTTAAC 1055
QY 1029 TAAAAATTTACACATCGATTGGCGTTGGGTGCAAAAATACTTTCAAAAATGTTGATTGA 1088
Db 1056 TAAAGATCTTTTATGTGATTGGCGTTTAGGAGAGCAGTATTTTCAACAACTAATTTGA 1115
QY 1089 CTATGATGCTGCAATATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGAACGGAGCG 1148
Db 1116 TTATGATGCTGCAGTATATCGGAGATGGCAGTGGGCTGCTTCCACTGGAAACAGATGC 1175
QY 1149 TGTCCCTTATTTTCGGATTTTAAATCCAAATATCCAGTCAAAAAATTTGATAATGACGG 1208
Db 1176 TGTTCCTTATTTTGAATATTTAAATCTGTACTCAAGTAAGCGCTTTGATCCTTAAAGG 1235
QY 1209 CCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCACAAAGTATATTCATCA 1268
Db 1236 CGAGTTTATTAAGCGTATTTTGCCTCACTAGAACACGTTCCAGAGAAGTATCTCCAGA 1295
QY 1269 ACCAAATCTAATGAACGAAGCCTTACAAACGCAATATCATGTATCATTTAGGAGAAAAATTA 1328
Db 1296 ACCGTGGAAGATGCCAAAAAACCTTCAGAGAGTGTCTGTATTTATTTGGCAGACTA 1355
QY 1329 TCCAAACCCCATTTGCGATTATGCAATCAAGTAAAAAACAACATTTGTTCTATATGAAGC 1388
Db 1356 TCTCAACCAATTTGTCATCATGCTAAACAACGTAACGTAACGCTATTGCAAAAGTATGAGTG 1415
QY 1389 GAGCAAGAAA 1399
Db 1416 GGCAAAAGAAA 1426
```

RESULT 13

ADF03864

ID ADF03864 standard; DNA; 1446 BP.

XX

AC

ADF03864;

XX

DT 12-FEB-2004 (first entry)

XX

DE

XX

KW Bacterial polynucleotide #4149.

XX

KW Proteus mirabilis infection; bacterial infection; antibacterial;

XX

KW immunostimulant; gene; ds.

XX

OS Proteus mirabilis.

XX

XX

PN US6605709-B1.

XX

PD 12-AUG-2003.

PF 05-APR-2000; 2000US-00543681.

XX

PR 09-APR-1999; 99US-0128706P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Breton GL;

XX

XX WPI; 2003-895291/82.

DR P-PSDB; ADF08036.

XX

XX New Proteus mirabilis polypeptides and polynucleotides, useful as

PT reagents for diagnosis of bacterial disease, as components of

PT antibacterial vaccines, as targets for antibacterial drugs, or as

PT biocontrol agents for plants.

XX

PS Disclosure; SEQ ID NO 4149; 870pp; English.

XX

XX The invention relates to new Proteus mirabilis polypeptides and

CC polynucleotides. The invention also relates to antibodies against the

CC polypeptides, methods for producing the polypeptides, a method of

CC generating vaccines for immunising an individual against P. mirabilis, a

CC method for evaluating a compound for the ability to bind a P. mirabilis

CC polypeptide and a method for screening test compounds for anti-bacterial

CC activity. The polypeptides and polynucleotides are useful as molecular

CC targets for diagnosing, preventing and treating pathological conditions

CC resulting from bacterial infection, as reagents for diagnosis of

CC bacterial diseases, as components of antibacterial vaccines, as targets

CC for antibacterial drugs or as bio-control agents for plants. This

CC sequence represents a Proteus mirabilis polynucleotide of the invention.

XX

SQ Sequence 1446 BP; 418 A; 321 C; 287 G; 420 T; 0 U; 0 Other;

XX

XX Query Match 14.8%; Score 212.2; DB 10; Length 1446;

XX

XX Best Local Similarity 60.0%; Pred. No. 7.9e-43;

XX

XX Matches 418; Conservative 0; Mismatches 258; Indels 21; Gaps 3;

XX

QY 596 GCGAAGAAACAGCAGAGCGCTTAAATACCTTTTATTGATCAAAAACTTCAATCCTATG 655

Db 635 GCGAACAAGCAGCGTTACAGCGTTTAAACAGTTTGTGATGAAAGGTGATACATTATG 694

QY 656 AAAATAAGCGTGATTTTCCTTATCAGGATCAACAGAGTCATCTGCTACTTTTTTAAGAA 715

Db 695 CAAAATGCGAGATATTCCTGATGTAAGCAACAGTCAATATATCCCTTATCTTGGCA 754

QY 716 CGGAGAACTTTGATTCGCACCATTTGGCAAGAGCTTGC---ATCTGTGCTTCTAGCT 772

Db 755 TAGGCCTAGTGTGTGCGCAATGTTTTTAATACGCTTTTACCNAACAGAGCCTGATTTCT 814

QY 773 TAAGTAAAGAAACCTTCAAA-----AAAGAAATTAGCTTTGGCGCGACTTTT 817

Db 815 TAGAAAATAACCATTCAGTGCATTTGTTTGGTTTAAATAGTATGTTTGGCGCGAGTTT 874

QY 818 ---ACAATATGATCTATAGTGGTTTCCAAACAAAAGAGAGAGCTATTCAAGAAAAAT 874

Db 875 ATCAACATCTAATAGTTGCTAAACCGAGTTTATCCAAACAGATAGCTTTTCAACCATGGA 934

QY 875 TTCGTTATTTCAATGGCAAAATGACCCAGAAATGTTTGTCAAGTGGCAAAAGGGGAGA 934

Db 935 CAGAAAATATTCGCTGGCGTAAATGACCAAACTGAATTTACCGCTTGGACACAGGGCTTAA 994

QY 935 CGGGGTACCTTATTAATGATGCGCAATGCGCAAACTGAATCAAACTGGTTGGATGCGACA 994

Db 995 CAGGCTTTCCTATTATGATGCGCGATGCGCACTGAATCAAAACCGCTGATGCGACA 1054

QY 995 ATCGCTTAAGAATGATTAAGTCTCTCTTTTATAGTTTAAATAATTACATCGATTGCGGTT 1054

Db 1055 ATCGCTTACGTATGCTGACGGCAAGTTTTTTTAGTCAAAAGATCTATTAATTTGATGCGCT 1114

QY 1055 GGGGTGAAAAATACCTTTCAAAAAATGTTGATGACTATGATGCTGCCAATATATCGGTG 1114

Db 1115 GGGGGGAAAAATTTATTTTATGTCACAAATTAATTTGGTGGTATTCGCTCAAAATAATGGTG 1174

QY	1115	GCTGGCAATGGCTCTTCAACAGGAACGCGCTGCTCCCTTATTTTCGGATTTTAAATC	1174
Db	1175	GCTGGCAATGGCTGCGATCAACAGGCACGTGATGCTGTGCTTATTTTCGGATTTTAAATC	1234
QY	1175	CAATTTATCCAGTCAAAAAAATTTGATTAATGACGGCCAGTTTCATCAAAAAAATATGTTCCAG	1234
Db	1235	CGACAACCCAGGACGTAAGTTTGATCCTGATGGTGAAGTTATCCGGCCACTGGCTACCAG	1294
QY	1235	AACCTAAGCAAGTGCACAAAGTATATTCATCAACC	1271
Db	1295	AGCTTGTGCTGATGCCAGATCGCTATATCCATACTCC	1331
RESULT 14			
ID	ACF74095	2003-120786/11.	
AC	ACF74095	standard; DNA; 1389 BP.	
XX	AC	ACF74095;	
XX	AC	ACF74095;	
DT	20-NOV-2003	(first entry)	
XX	XX	Staphylococcus aureus DNA #1775.	
DE	XX	Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;	
XX	XX	enzymatic assay; antibiotic target; gene; ds.	
KW	XX	Staphylococcus aureus.	
XX	OS	WO200294868-A2.	
XX	PN	28-NOV-2002.	
XX	PD	27-MAR-2002; 2002MO-IB002637.	
PF	XX	27-MAR-2001; 2001GB-00007661.	
XX	PR	(CHIR-) CHIRON SPA.	
XX	PA	Maignani V, Mora M, Scarselli M;	
PI	XX	WPI; 2003-120786/11.	
DR	XX	P-PSDB; ABM72535.	
XX	XX	New Staphylococcus aureus protein, useful as a vaccine for treating or	
PT	XX	preventing Staphylococcal infection, specifically an infection caused by	
PT	XX	S. aureus, e.g. sepsis.	
XX	XX	Claim 6; SEQ ID NO 3549; 49pp; English.	
PS	XX	The invention relates to novel genes and encoded proteins from	
CC	XX	Staphylococcus aureus. A composition comprising the S. aureus protein, a	
CC	XX	nucleic acid encoding the protein, or an antibody to the protein, is	
CC	XX	useful as a pharmaceutical, particularly as a vaccine for treating or	
CC	XX	preventing infection due to Staphylococcus bacteria, specifically an	
CC	XX	infection caused by S. aureus. The composition is particularly useful for	
CC	XX	treating or preventing sepsis in a patient. The composition can also be	
CC	XX	used for diagnostics. The protein is also used in an assay for enzymatic	
CC	XX	studies and as a target for antibiotics. This sequence represents one of	
CC	XX	the novel S. aureus genes of the invention	
XX	XX	Sequence 1389 BP; 471 A; 210 C; 261 G; 447 T; 0 U; 0 Other;	
SQ	XX	Query Match 14.4%; Score 206.2; DB 8; Length 1389;	
XX	XX	Best Local Similarity 56.2%; Pred. No. 2.5e-41;	
XX	XX	Matches 432; Conservative 0; Mismatches 328; Indels 9; Gaps 2;	
QY	627	TTTTATTATCAAAAACCTTCAATCCATGAAATAAGGTGATTTTCTTATCAGGATCA	686
Db	618	TTTTTTAGATCAAGATATACAGAAATAGAAAGCGGAAGACATTTACCTGAAGATT	677
QY	687	AACGAGTCATCTGCTACTTTTAAAGAAACGGGAGAACTTTTCGATTCGCACCATTTGGCA	746
Db	678	AACAAGTCAGCTAAGTGTGCTTTAGCATATGGATTATTAGATATTATTGAAATTTTAA	737

QY	747	AGT-----GCTTGCATCTGTGCTTCTAGCTTAAAGTAAGAACCTTCAAAAAAGAAATT	800
Db	738	TGATTTATTGGCCCGTTATGATGAAGATGAGGCAAACTATGAAGCAATTTATAGCTGAAT	797
QY	801	AGCTTGGCGGACCTTTTACAATATGATCTATAGTGGGTTTCCACAACAAAAAGAGGAAGC	860
Db	798	CATTTTATAGAGATTTTATTAATGTTAATGACACAGTATCTCTGAAACCTCATACCAAGC	857
QY	861	TATTCAAGAAAAATTTTCGTTATATTCAATGGACAAATGACCCAGAAATGTTTGTCTAAGTG	920
Db	858	TTTCAAAACCTAAATATCGACAGATAAAATGGTCGCAAAATGAAGCGGATTTTAAATGCATG	917
QY	921	GCAAAAGGGGAGACGGGTACCTATTAATGATGCGGAATGGCACTGATCAATCAAAAC	980
Db	918	GTGCGAAGGGCAACAGGATTTTCAATCATTTGATGAGCAATAATGGAATTTGACACAAAC	977
QY	981	TGGTTGGATGCACAATCGCTTAAGAATGATTACTGCTCTTTTAAAGTTTAAATAATTACA	1040
Db	978	TGGTTTATGTCATTAATCGAATGGAATGGTTGTGCGCAATTTTAAACCAAGATTTATT	1037
QY	1041	CATCGATTGGCGTTGGGGTGAATAATCATTTTCAAAAAATGTTGATTGACTATGATGCTGC	1100
Db	1038	TATAGATTGGACATGGGAGAAAAATTTCTTTAGAAAGCACCTTATTGACTATGATGCGAGC	1097
QY	1101	CAATATATCGGTGGCTGCAATGGCTGCTTCAACAGGAACGAGCGCTGCTCCCTTATTT	1160
Db	1098	ATCAATAATTTGATGGATGGCAATGGTCTGCTTCTACAGGTACGATGCGATGCGGTAAT	1157
QY	1161	TCGGATTTTAAATCCAAATATCCAGTCAAAAAAATTTGATAATGACGGCCAGTTTCATCAA	1220
Db	1158	TAGATGTTTAAATCCAAATAGACAGAGTGAACGCTTTGATGCTTAAAGCTTTGTATATCAA	1217
QY	1221	AAAATATGTTCCAGAACTTAAGCAAGTGCCACAAGATATATTTCATCAACCAATCTAAT	1280
Db	1218	AACATATCTCCGATTTTAAATCAAAATGATGCAAAATATTTGCATGATACA---CAACG	1274
QY	1281	GAACGAAGCTTTACAAACGCAATATCATGTACATTTAGGAGAAAAATATCCAAAAACCAT	1340
Db	1275	CAATGATCCAACTTTTGAACAGGGGATTTAGGTAGTGCATTTATCAATTTAAAGCG	1334
QY	1341	TGTGATTTATGCATCAAGTAAAAAACAACATTTGTTTCTATATGAAGCG	1389
Db	1335	GGTAGATCATCAAGAAAAACGTACACAGTTTATAGTACATTTTAAAGCG	1383
RESULT 15			
ID	AAV74905	AAV74905 standard; DNA; 1393 BP.	
XX	AC	AAV74905;	
XX	DT	16-MAR-1999 (first entry)	
XX	DE	Staphylococcus aureus contig SEQ ID #594.	
XX	XX	Computer readable medium; vaccine; S. aureus infection; immunodetection;	
KW	XX	cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;	
KW	XX	skin infection; surgical wound infection; scalded skin syndrome;	
KW	XX	toxic shock syndrome; ds.	
XX	OS	Staphylococcus aureus.	
XX	XX	Key Location/Qualifiers	
PH	XX	misc_feature 61..120	
FT	XX	/*tag= a	
FT	XX	/note= "these bases represent a line of missing text in	
FT	XX	the sequence listing in the specification. They are	
FT	XX	included to maintain the nucleotide numbering given in	
FT	XX	the specification for this DNA sequence"	
PN	XX	EP786519-A2.	
XX	XX	XX	

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